

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	1321	100.0	1321	6	AX392417	Sequence	AX392417 Sequence
2	1229	93.0	4839	6	C0812357	Sequence	C0812357 Sequence
3	1229	93.0	4839	6	AF305616	Homo sapi	AF305616 Homo sapi
4	1227.4	92.9	1383	6	AX775889	Sequence	AX775889 Sequence
5	887.4	67.2	1061	9	BC015918	Homo sapi	BC015918 Homo sapi
6	861	65.2	861	6	AX392419	Sequence	AX392419 Sequence
7	803.2	60.8	969	6	BD272494	Secreted	BD272494 Secreted
8	802.2	60.7	1141	9	AF224278	Homo sapi	AF224278 Homo sapi
9	801.8	60.7	1913	6	BD272544	Secreted	BD272544 Secreted
10	801.6	60.7	969	6	BD272534	Secreted	BD272534 Secreted
11	801.6	60.7	969	6	BD272515	Secreted	BD272515 Secreted
12	801.6	60.7	969	6	BD272516	Secreted	BD272516 Secreted
13	801.6	60.7	1140	6	AX336830	Sequence	AX336830 Sequence
14	800.6	60.6	1085	6	AX775887	Sequence	AX775887 Sequence
15	800	60.6	1818	9	AY128643	Homo sapi	AY128643 Homo sapi
16	797.4	60.4	1060	6	BC080635	Homo sapi	BC080635 Homo sapi
17	755.8	57.2	759	6	AX336831	Sequence	AX336831 Sequence
18	755.4	57.2	759	6	BD272545	Secreted	BD272545 Secreted
19	751.2	56.9	756	6	BD272495	Secreted	BD272495 Secreted

QY	61	CGGCGGCGGCGGCGGCGGAGCGCTCGGCTGGGGAAGCTAGCGGCAAGGCTCAGCCCC	120
DB	61	CGGCGGCGGCGGCGGCGGAGCGCTCGGCTGGGGAAGCTAGCGGCAAGGCTCAGCCCC	120
QY	121	GGCGGAGCGCGCGCCCGCTGCGAGCCCATTTTCCGAGCCCAACCCCGCGGCACTGCGG	180
DB	121	GGCGGAGCGCGCGCCCGCTGCGAGCCCATTTTCCGAGCCCAACCCCGCGGCACTGCGG	180
QY	181	ACGCCCCGCGGCTGCGCAGAGGAGGCGCGGCGGCGCGAGCGGAGCGGCTCCCGCGCAC	240
DB	181	ACGCCCCGCGGCTGCGCAGAGGAGGCGCGGCGGCGCGAGCGGAGCGGCTCCCGCGCAC	240
QY	241	TGAGCCCCGCGCGCCCGCGGAACTTTGGCGCGACCCCGAGCCCGCGAGCCGCGGCGCGC	300
DB	241	TGAGCCCCGCGCGCCCGCGGAACTTTGGCGCGACCCCGAGCCCGCGAGCCGCGGCGCGC	300
QY	301	CTCCCCCGCGCGCCTCTGCTGATGGGGCCCCAGCTCCGGGCGCGCGCGCGAGGCCCC	360
DB	301	CTCCCCCGCGCGCCTCTGCTGATGGGGCCCCAGCTCCGGGCGCGCGCGCGAGGCCCC	360
QY	361	CCCGCGCGCCCGCGAGCCCCCGCGCCCCCGCGCGCGCGCGCTCCATGCAACG	420
DB	361	CCCGCGCGCCCGCGAGCCCCCGCGCCCCCGCGCGCGCGCTCCATGCAACG	420
QY	421	CTTGATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCTCTCTGAC	480
DB	421	CTTGATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCTCTCTGAC	480
QY	481	GTGCAACTGCAAACGCTTTGTTTCAGAGCATGAGATCACGAGCTGGAGTTGTTCA	540
DB	481	GTGCAACTGCAAACGCTTTGTTTCAGAGCATGAGATCACGAGCTGGAGTTGTTCA	540
QY	541	GATCATCATCATCGTGGTGGTGAATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	600
DB	541	GATCATCATCATCGTGGTGGTGAATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG	600
QY	601	CCACTACAAGCTGTCTGCAAGGCTCTTCATCAGCCGGCAACGCGGCGGAGAGAGA	660
DB	601	CCACTACAAGCTGTCTGCAAGGCTCTTCATCAGCCGGCAACGCGGCGGAGAGAGA	660
QY	661	AGATGCCCTGTCTCAGAAAGATGCCGTGGCCCTCGGAGAGCACAGTGTGAGCAACGG	720
DB	661	AGATGCCCTGTCTCAGAAAGATGCCGTGGCCCTCGGAGAGCACAGTGTGAGCAACGG	720
QY	721	AATCCAGAGCCGAGTCTACGCCCGCTCGGCCCAACCGCGCTGGCGCTGCGCGCC	780
DB	721	AATCCAGAGCCGAGTCTACGCCCGCTCGGCCCAACCGCGCTGGCGCTGCGCGCC	780
QY	781	CTTCGCCAGGGGAGCGCTTCCACCGCTTCAGCCCACTATCTGCTACTGAGCAGCA	840
DB	781	CTTCGCCAGGGGAGCGCTTCCACCGCTTCAGCCCACTATCTGCTACTGAGCAGCA	840
QY	841	GATCGACTGCACCCACCATCTCGCTGTAGAGGGGAGAGCCCCACCCCTACCAAGG	900
DB	841	GATCGACTGCACCCACCATCTCGCTGTAGAGGGGAGAGCCCCACCCCTACCAAGG	900
QY	901	CCCTGCACTCGCTTCAGTTTCGGGACCCGAGCAGCAGCTGAACTGAACCGGGAGTCCGT	960
DB	901	CCCTGCACTCGCTTCAGTTTCGGGACCCGAGCAGCAGCTGAACTGAACCGGGAGTCCGT	960
QY	961	GGCGGCAACCCCAACAGAACCATCTTTCGACAGTGAACCTGATGATGTCAGGCTGGG	1020
DB	961	GGCGGCAACCCCAACAGAACCATCTTTCGACAGTGAACCTGATGATGTCAGGCTGGG	1020
QY	1021	CGGCCCCCTGCCCCCGCAGCAGTAACCTCGGGCATCAGCGCCACGCTGCTACCGCAGCGCGG	1080
DB	1021	CGGCCCCCTGCCCCCGCAGCAGTAACCTCGGGCATCAGCGCCACGCTGCTACCGCAGCGCGG	1080
QY	1081	GGCGATGAGGGGCGCGCCCACTTACGCGAGGTCATCGGCACTACCGGGGCTCTC	1140
DB	1081	GGCGATGAGGGGCGCGCCCACTTACGCGAGGTCATCGGCACTACCGGGGCTCTC	1140

Qy	1141	CTTCCAGACACGACGAGCAGTGGCGCGCCTCTCTTGCTGGAGGGAGCCCGGTCTCACCA	1200
Db	1141	CTTCCAGCACCAGCAGCAGTGGCGCGCCTCTCTTGCTGGAGGGAGCCCGGTCTCACCA	1200
Qy	1201	CACACATCGCCCCCTAGAGACGCGACCATCTGGAGCAAAAGAGAGATAAACAGAA	1260
Db	1201	CACACATCGCGCCCCCTAGAGACGCGACCATCTGGAGCAAAAGAGAGATAAACAGAA	1260
Qy	1261	AGGACACCTCTCTTAGGGTCCCCCAGGGGGCGGGCTGGGGCTGCCTAGGTGAAAAAGGCA	1320
Db	1261	AGGACACCTCTCTTAGGGTCCCCCAGGGGGCGGGCTGGGGCTGCCTAGGTGAAAAAGGCA	1320
Qy	1321	G 1321	
Db	1321	G 1321	
RESULT 2			
CO812357			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
misc_feature			
ORIGIN			
Query Match			
Best Local Similarity 100.0%: Pred. No. 2,7e-163;			
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
Qy	93	GGAAAGCTAGCGCAGAGGCTCAGCCCCCGGCGCAGCGCGCCCGGTGCCAGCCCAATT	152
Db	1	GGAAAGCTAGCGCAGAGGCTCAGCCCCCGGCGCAGCGCGCCCGGTGCCAGCCCAATT	60
Qy	153	TTCCGAGCCACCCCGGGGCTGCGAGCGCCCCCGGGGCTGCCGAGGGAGGCGCGGG	212
Db	61	TTCCGAGCGCACCCCGGGGCTGCGAGCGCCCCCGGGGCTGCCGAGGGAGGCGCGGG	120
Qy	213	GGCGCAGCGGAGCGCGGTCCCGCGCAGCTAGAGCCCCCGGGCGCCCCGGGAACTTGGCGGC	272
Db	121	GGCGCAGCGGAGCGCGGTCCCGCGCAGCTAGAGCCCCCGGGCGCCCCGGGAACTTGGCGGC	180
Qy	273	GACCCGAGCTCCGCGAGCGGGGCGCGCTCCCTCCCGCGCGCGCTCTCTGATGCGGGGC	332
Db	181	GACCCGAGCTCCGCGAGCGGGGCGCGCTCCCTCCCGCGCGCGCTCTCTGATGCGGGGC	240
Qy	333	CCAGCTCCGGGGCGCGGGAGCCCCCGCGGGCGCCCCCGAGCCCCCGCGCCCCCGC	392
Db	241	CCAGCTCCGGGGCGCGGGAGCCCCCGCGGGCGCCCCCGAGCCCCCGCGCCCCCGC	300
Qy	393	GCCGCGCGCGCGCTCCATGACCGCTTGATGGGGTCAACAGCACCGCGCGCGCG	452
Db	301	GCCGCGCGCGCGCTCCATGACCGCTTGATGGGGTCAACAGCACCGCGCGCGCG	360
Qy	453	CCGCCGGGAGGCCAATGTCTCTGCACTGCAACTGCAAAACGCTCTTTGTTCCAGAGCA	512


```
/codon_start=1
/product="PMEP1 protein"
/protein_id="AAF86322.1"
/db_xref="GI:9255809"
/translation="MAELFEVOLIIVVMVVMVITCLSHYKLSBSFISRHQS
RRREDALSEGCLWPSESTVSGNGIEBPQYAPPRTRDLAVPPFAQRERFHRFQTY
PYLQHEIDLPPTLSLSDGEPPEPPYQGFCTQLQDPEQLNRESVRAPNRTIFDSD
LMDASRLGFCPPSSNGISATCYSGSGMEGPPPTYSVIGHYPPGSSPQHOSSGPP
SLLEGTRLHHHTIAPLESAAIWSKENDKQKQHPL"
ORIGIN
Query Match      60.7%; Score 802.2; DB 9; Length 1141;
Best Local Similarity 98.4%; Pred. No. 2.8e-103;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
QY 499 TTTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTGTTTCATCATCATCATCATCGTGGT 558
Db 77 TCTCTCGGNAACAGGCAATGGCGAGCTGGAGTTGTTTCATCATCATCATCATCGTGGT 136
QY 559 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618
Db 137 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 196
QY 619 ACSTGCTTTCATCAGCGGACAGCCAGCGGGCGGAGAGAGATGCCCTGTCTCAGA 678
Db 197 ACSTGCTTTCATCAGCGGACAGCCAGCGGGCGGAGAGAGATGCCCTGTCTCAGA 256
QY 679 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 738
Db 257 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 316
QY 739 CTACGCGCCGCTCGGCGCCACCGACCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 798
Db 317 CTACGCGCCGCTCGGCGCCACCGACCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 376
QY 799 CTTCCACCGCTTCAGCGCCACCTATCGGTACCTGCGAGCAGAGATCGAAGCTGCGACCCAC 858
Db 377 CTTCCACCGCTTCAGCGCCACCTATCGGTACCTGCGAGCAGAGATCGAAGCTGCGACCCAC 436
QY 859 CATCTCGCTGTCAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 918
Db 437 CATCTCGCTGTCAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 496
QY 919 TCGGAGACCCCGAGCAGAGCTGGAACCTGAAACCGGGAGTGGTGGCGGCGACCCCGCAACAG 978
Db 497 TCGGAGACCCCGAGCAGAGCTGGAACCTGAAACCGGGAGTGGTGGCGGCGACCCCGCAACAG 556
QY 979 AACCATCTTCGACAGTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1038
Db 557 AACCATCTTCGACAGTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 616
QY 1039 CAGTAACCTGGGCATCAGCGCCACGCTGCTACGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 1098
Db 617 CAGTAACCTGGGCATCAGCGCCACGCTGCTACGCGAGCGGCGGCGGCGGCGGCGGCGGCGG 676
QY 1099 GCCACCTACAGCGAGTCACTCGGCCACTACCGCGGGTCTCTCTCCAGCAGCAGCAGAG 1158
Db 677 GCCACCTACAGCGAGTCACTCGGCCACTACCGCGGGTCTCTCTCCAGCAGCAGCAGAG 736
QY 1159 CAGTGGCGCGCTCTCTCTGTCGAGGGGACCGCGCTCCACACACACATGCGCGCT 1218
Db 737 CAGTGGCGCGCTCTCTCTGTCGAGGGGACCGCGCTCCACACACACATGCGCGCT 796
QY 1219 AGAGCGGAGCATCTGGAGCAAGAGAGAGATTAACGAAAGGACACCTCTCTTAGG 1278
Db 797 AGAGCGGAGCATCTGGAGCAAGAGAGAGATTAACGAAAGGACACCTCTCTTAGG 856
QY 1279 TCCCCAGGGGGCGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 1321
Db 857 TCCCCAGGGGGCGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 899
FEATURES
source
Location/Qualifiers
1..1913
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match      60.7%; Score 801.8; DB 6; Length 1913;
Best Local Similarity 98.3%; Pred. No. 2.8e-103;
Matches 809; Conservative 1; Mismatches 13; Indels 0; Gaps 0;
QY 499 TTTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTGTTTCATCATCATCATCATCGTGGT 558
Db 127 TCTCTCGGNAACAGGCAATGGCGAGCTGGAGTTGTTTCATCATCATCATCATCGTGGT 186
QY 559 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 618
Db 187 GGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 246
QY 619 ACSTGCTTTCATCAGCGGACAGCCAGCGGGCGGAGAGAGATGCCCTGTCTCAGA 678
Db 247 ACSTGCTTTCATCAGCGGACAGCCAGCGGGCGGAGAGAGATGCCCTGTCTCAGA 306
QY 679 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGT 738
Db 307 AGGATGCTGTGCTCGGAGAGCAGTGTGAGCAAGCAAGCAAGCAAGCAAGCAAGT 366
QY 739 CTACGCGCCGCTCGGCGCCACCGACCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 798
Db 367 CTACGCGCCGCTCGGCGCCACCGACCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCGCTGGCG 426
QY 799 CTTCCACCGCTTCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 858
Db 427 CTTCCACCGCTTCAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 486
QY 859 CATCTCGCTGTCAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 918
Db 487 CATCTCGCTGTCAGCGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGT 546
QY 919 TCGGAGACCCCGAGCAGCAGTGAACCTGAAACCGGGAGTGGTGGCGGCGACCCCGCAACAG 978
Db 547 TCGGAGACCCCGAGCAGCAGTGAACCTGAAACCGGGAGTGGTGGCGGCGACCCCGCAACAG 606
QY 979 AACCATCTTCGACAGTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1038
```

```
Db 607 AACATCTTTCGACAGTACCTGATGATAGTCAGGCTGGGCGCCCTTGCCTCCCGCCAG 666
QY 1039 CAGTAATCTGGGATCAGCGCCACGCTGCTACGCGCAGCGGCGCGCGCATGAGGCGCGCC 1098
Db 667 CAGTAATCTGGGATCAGCGCCACGCTGCTACGCGCAGCGGCGCGCGCATGAGGCGCGCC 726
QY 1099 GCCACCTACAGCGAGGTATCTGGGCACTACCCCGGGTCTCTTCCAGCACGAGCAGAG 1158
Db 727 GCCACCTACAGCGAGGTATCTGGGCACTACCCCGGGTCTCTTCCAGCACGAGCAGAG 786
QY 1159 CAGTGGCGCGCCCTCTCTGCTGAGGGGACCGGCTCCACACACACATCGCGCCCT 1218
Db 787 CAGTGGCGCGCCCTCTCTGCTGAGGGGACCGGCTCCACACACACATCGCGCCCT 846
QY 1219 AGAGAGCGAGCCATCTGAGGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGG 1278
Db 847 AGAGAGCGAGCCATCTGAGGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGGG 906
QY 1279 TCCCCAGGGGCGCGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1321
Db 907 TCCCCAGGGGCGCGGCTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 949

RESULT 10
BD272514
LOCUS
DEFINITION
SECRETED proteins and nucleic acids encoding them.
ACCESSION
BD272514
VERSION
BD272514.1 GI:33082282
KEYWORDS
JP 2002539773-A/23.
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 969)
Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 23 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002539773-A/23
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES,DOUGLAS A HOLTZMAN, JOHN D SHARP,CHRISTOPHER C
PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
GOIN33/15,
PC GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00 CC
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
FT CDS Location/Qualifiers
source
1..969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 60.7%; Score 801.6; DB 6; Length 969;
Best Local Similarity 99.5%; Pred. No. 3.4e-103;
Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 514 GGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGTGATGTGAT 573
Db 2 GGAGATGCGCGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGTGATGTGAT 61
QY 574 GGTGGTGGTGTATCATCGTGTCTGAGGCCACTACAAGCTGTCTGACGGTCTTTCATCAG 633
Db 62 GGTGGTGGTGTATCATCGTGTCTGAGGCCACTACAAGCTGTCTGACGGTCTTTCATCAG 121
QY 634 CCGGCACAGCCAGGGGCGGAGAGAGATGCCCTGTCTCAGAGAGGATGCCGTGTGGCC 693
```

```
Db 122 CCGGCACAGCCAGGGGCGGAGGAGAGATGCTCTCTCAGAGGATGCTGTGGCC 181
QY 694 CTCGAGAGACACAGTGTCTCAGGGCAACCGAATCCAGAGCCGCGAGTCTACGCCCGCGCTCG 753
Db 182 CTCGAGAGACACAGTGTCTCAGGGCAACCGAATCCAGAGCCGCGAGTCTACGCCCGCGCTCG 241
QY 754 GCCACCGAGCCGCTGGCGCTGGCGCTTTCGCGCCAGCGGGAGCGTCTCCACCGCTTCCA 813
Db 242 GCCACCGAGCCGCTGGCGCTGGCGCTTTCGCGCCAGCGGGAGCGTCTCCACCGCTTCCA 301
QY 814 GCCACCTATTCGTACTCTGACGACGAGATCGACCTGCGCCACCATCTCGCTGTCTCAG 873
Db 302 GCCACCTATTCGTACTCTGACGACGAGATCGACCTGCGCCACCATCTCGCTGTCTCAG 361
QY 874 CCGGGAGGAGCCCGCCACCTACAGGGCGCTTGCACCTCTCGAGCTTCGGAGCCCGGAGCA 933
Db 362 CCGGGAGGAGCCCGCCACCTACAGGGCGCTTGCACCTCTCGAGCTTCGGAGCCCGGAGCA 421
QY 934 GCAGCTGGAACTGAACCCGGAGTGTGGTGGCGCACCCCCCAACAGAAACCATCTTCGACAG 993
Db 422 GCAGCTGGAACTGAACCCGGAGTGTGGTGGCGCACCCCCCAACAGAAACCATCTTCGACAG 481
QY 994 TGACCTGATGGATAGTGCAGGCTGGCGCGCCCTGCGCCCGCCAGCAGTAACCTCGGGCAT 1053
Db 482 TGACCTGATGGATAGTGCAGGCTGGCGCGCCCTGCGCCCGCCAGCAGTAACCTCGGGCAT 541
QY 1054 CAGCGCCAGCTGTCTACGCGAGCGGGCGGCGCATGAGAGGGCGCCGCCACCATCTACAGCGA 1113
Db 542 CAGCGCCAGCTGTCTACGCGAGCGGGCGGCGCATGAGAGGGCGCCGCCACCATCTACAGCGA 601
QY 1114 GGTCTATCGGCCACTACCCGGGGTCTCTTCAGACACACAGAGAGAGTGGGCGCGCTC 1173
Db 602 GGTCTATCGGCCACTACCCGGGGTCTCTTCAGACACACAGAGAGAGTGGGCGCGCTC 661
QY 1174 CTTGCTGAGGGGACCCCGCTCCACACACACATCGGCGCCCTTAGAGAGCGCAGCAT 1233
Db 662 CTTGCTGAGGGGACCCCGCTCCACACACACATCGGCGCCCTTAGAGAGCGCAGCAT 721
QY 1234 CTGGAGCAAGAGAGAGGATAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1293
Db 722 CTGGAGCAAGAGAGAGAGGATTAACAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 781
QY 1294 GGCTGGGGCTGCTGCTAGGTGAAAAGGCGAG 1321
Db 782 GGCTGGGGCTGCTGCTAGGTGAAAAGGCGAG 809

RESULT 11
BD272515
LOCUS
DEFINITION
SECRETED proteins and nucleic acids encoding them.
ACCESSION
BD272515
VERSION
BD272515.1 GI:33082283
KEYWORDS
JP 2002539773-A/24.
Homo sapiens (human)
SOURCE
Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 969)
Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 24 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002539773-A/24
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES,DOUGLAS A HOLTZMAN, JOHN D SHARP,CHRISTOPHER C
PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
GOIN33/15,
```

PC G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N15/00 CC
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers (6). (761).
FT CDS Location/Qualifiers
source 1..969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
ORIGIN
Query Match 60.7%; Score 801.6; DB 6; Length 969;
Best Local Similarity 99.5%; Pred. No. 3.4e-103;
Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 514 GGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGATGTGAT 573
DB 2 GGAGATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGATGTGAT 61

QY 574 GTGTGTGTGATCAGCTGCTGCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 633
DB 62 GTGTGTGTGATCAGCTGCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 121

QY 634 CCGGCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTGTGGCC 693
DB 122 CCGGCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTGTGGCC 181

QY 694 CTGCGAGAGCAGTGTCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 753
DB 182 CTGCGAGAGCAGTGTCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 241

QY 754 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 813
DB 242 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 301

QY 814 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 873
DB 302 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 361

QY 874 CCGGCAGAGGAGCCCGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 933
DB 362 CCGGCAGAGGAGCCCGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 421

QY 934 GCAGCTGGAATGAACCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAG 993
DB 782 GGCTGGGGTCTGCTAGGTGAAAGGCGAG 1321
GGCTGGGGTCTGCTAGGTGAAAGGCGAG 809

BD272516
LOCUS
DEFINITION
SECRETED proteins and nucleic acids encoding them.
ACCESSION
BD272516
VERSION
BD272516.1 GI:33082284
KEYWORDS
JP 2002539773-A/25.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 969)
Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 25 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT
OS Homo sapiens (human)
PN JP 2002539773-A/25
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
PI FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12O1/68, PC
G01N33/15,
G01N33/50, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers (6). (761).
FT CDS Location/Qualifiers
source 1..969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

FEATURES
source
ORIGIN
Query Match 60.7%; Score 801.6; DB 6; Length 969;
Best Local Similarity 99.5%; Pred. No. 3.4e-103;
Matches 804; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 514 GGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGATGTGAT 573
DB 2 GGAGATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGATGTGAT 61

QY 574 GTGTGTGTGATCAGCTGCTGCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 633
DB 62 GTGTGTGTGATCAGCTGCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 121

QY 634 CCGGCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTGTGGCC 693
DB 122 CCGGCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTGTGGCC 181

QY 694 CTGCGAGAGCAGTGTCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 753
DB 182 CTGCGAGAGCAGTGTCTGAGCCACTAAGCTGTCTGCAAGCTGCTTTCATCAG 241

QY 754 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 813
DB 242 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 301

QY 814 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 873
DB 302 GCGCCACAGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 361

QY 874 CCGGCAGAGGAGCCCGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 933
DB 362 CCGGCAGAGGAGCCCGCCAGCGGCGGAGGAGAGATGCTGCTCAGAGGATGCTTTCATCAG 421

QY 934 GCAGCTGGAATGAACCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAG 993
DB 422 GCAGCTGGAATGAACCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAG 1053
TGACCTGTGATGATGTCGCGGCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAGTCTGGTGGCGGAG

Db	704	GCCTACTACCGGGTCTCTCTCCAGCACACAGAGAGAGTGGGCGCCCTCTTGTGG	763
QY	1182	AGGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGAGCCATCTGGAGCA	1241
Db	764	AGGGGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGAGCCATCTGGAGCA	823
QY	1242	AAGAGAAGGATAAACAGAAAGGACCCCTCTTAGGGTCCCCAGGGGGCGGGCTGGGG	1301
Db	824	AAGAGAAGGATAAACAGAAAGGACCCCTCTTAGGGTCCCCAGGGGGCGGGCTGGGG	883
QY	1302	CTCGTAGGTGAAAAGGCAG	1321
Db	884	CTCGTAGGTGAAAAGGCAG	903

Search completed: February 19, 2005, 14:21:11
Job time : 5705.7 secs

This Page Blank (uspro)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 00:48:19 ; Search time 707.116 Seconds
(without alignments)
11058.969 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcggagcga.....ctgcgtagtgtaaaagggcag 1321

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1321	100.0	1321	6	Abk12137 Human cdn
2	1301	98.5	4911	13	Acc40804 Tumour-as
3	1229	93.0	4839	8	Acc49552 Tumour-as
4	1229	93.0	4839	11	Adp65809 Human STA
5	1229	93.0	4839	11	Adp65729 Human tra
6	1229	93.0	4839	12	Adm67045 Human hom
7	1229	93.0	4839	13	Adr65875 Human pro
8	1229	93.0	4839	13	Adr66778 Human pro
9	1227.4	92.9	1383	10	Adc37326 Nuclear f
10	864	65.4	864	11	Adn38809 Cancer/an
11	803.2	60.8	969	3	Aaa75151 cDNA enco
12	802.2	60.7	1140	6	Abk92120 Prostate
13	802.2	60.7	1141	10	Adb75588 Prostate
14	802.2	60.7	1850	8	Acc49536 Tumour-as
15	802.2	60.7	4527	11	Adl83313 Human and
16	801.6	60.7	969	3	Aaa75164 cDNA clon
17	801.6	60.7	969	3	Aaa75163 cDNA clon
18	801.6	60.7	969	3	Aaa75165 cDNA clon
19	801.6	60.7	1140	10	Ado60105 Human and
20	801.6	60.7	1140	10	Adh62276 Human PME

21	801.6	60.7	1140	12	ADO39826	Ado39826 Human PME
22	800.6	60.6	1061	3	AAA47429	Aaa47429 Sequence
23	800.6	60.6	1085	10	ADC37324	Adc37324 Nuclear f
24	800.6	60.6	1334	8	ABZ36103	Abz36103 Human sec
25	790.4	59.8	1066	4	AAI57868	Aai57868 Human pol
26	767.4	58.1	806	8	ACC49537	Acc49537 Tumour-as
27	760	57.5	1069	4	AAI59654	Aai59654 Human pol
28	755.8	57.2	759	10	ADP17545	Adp17545 Human and
29	755.8	57.2	759	10	ADH62277	Adh62277 Human PME
30	755.8	57.2	759	12	ADO39827	Ado39827 Human PME
31	616.4	46.7	878	6	ABK12142	Abk12142 Mouse cdn
32	589.2	44.6	1583	6	ABSG61424	Absg61424 Prostate
33	493.6	37.4	593	6	ABK12143	Abk12143 Human MIV
34	466.2	35.3	1713	3	AAA75152	Aaa75152 cDNA enco
35	464.6	35.2	1713	3	AAA75167	Aaa75167 cDNA clon
36	464.6	35.2	1713	3	AAA75166	Aaa75166 cDNA clon
37	464.6	35.2	1713	3	AAA75168	Aaa75168 cDNA clon
38	417.8	31.6	812	2	AAZ52964	Aaz52964 Human pro
39	417	31.6	474	10	ABZ84732	Abz84732 Toxicolog
40	410.8	31.1	711	12	ADO00336	Ado00336 Novel hum
41	410.8	31.1	711	12	ADN98767	Adn98767 Novel hum
42	401.4	30.4	408	5	AAF65983	Aaf65983 Novel hum
43	400.6	30.3	673	6	ABT09178	Abt09178 Phase-1 R
44	400.6	30.3	673	12	ADG45576	Adg45576 Liver inf
45	400.6	30.3	673	12	ADH22874	Adh22874 Partial D

ALIGNMENTS

RESULT 1
ABK12137
ID ABK12137 standard; cDNA; 1321 BP.
XX
AC ABK12137;
XX
DT 05-JUN-2002 (first entry)
XX
DE Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.
XX
KW Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;
KW cytoskeletal; cardiant; cerebroprotective; antiarteriosclerotic;
KW cardiac cell; anti-apoptotic; vascular endothelial cell;
KW heart failure.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
CDS 413..1276
FT /*tag= a
FT /product= "MIVR-1"
FT /note= "This region is specifically claimed in claim 3"
XX
XX WO200216416-A2.
XX
XX 28-FEB-2002.
XX
XX 21-AUG-2001; 2001WO-US026089.
XX
XX 22-AUG-2000; 2000US-0227159P.
XX
XX (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
XX (PFIZ) PFIZER INC.
XX
XX Lee RT, Landschulz KT, Kennedy SP, Thompson JP, Turi TG;
XX WPI; 2002-280912/32.
XX P-PSDB; AAU78231.
XX
XX Novel nucleic acid molecule encoding Mechanically Induced Vascular
XX Receptor-1 polypeptide, useful for treating cardiovascular diseases.
XX

Claim 2; Page 87-88; 105pp; English.

The invention relates to an isolated nucleic acid molecule encoding a Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having a cardiac cell anti-apoptotic activity and fragments of it provided they are not identical to Genbank sequences A1761441.1, A1594390, NM 004338 and A0177461. Also included are expression vectors, host cells, the MIVR-1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting a molecule having cardiac cell anti-apoptotic activity with a candidate agent, where the molecule is a nucleic acid molecule comprising MIVR-1, IEX-1, VDP-1, BFG-2 and TIS-1 or its expression product, determining if the anti-apoptotic activity is modulated and thereby identifying a modulator. The cardiac cell anti-apoptotic molecules and nucleic acids of the invention are useful for treating, diagnosing and monitoring progression of such diseases and disorders as characterized by increased apoptotic cell-death of vascular endothelial cells e.g. cardiac hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart failure. The present sequence encodes human MIVR-1

Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 1321; DB 6; Length 1321;
Best Local Similarity 100.0%; Pred. No. 2.6e-198;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGCGGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGG 60
DB 1 CGACCGCGGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGG 60
QY 61 CGGCGGCGGCGGCGGAGCGCTCGCTGGGAAAGCTAGCGGCGAGGCTCAGCCCC 120
DB 61 CGGCGGCGGCGGCGGAGCGCTCGCTGGGAAAGCTAGCGGCGAGGCTCAGCCCC 120
QY 121 GCGCGAGCGCGCGCGCGCTGCGAGCCCATTTTCGAGCGCCACCGCGGCGGCGGCG 180
DB 121 GCGCGAGCGCGCGCGCGCTGCGAGCCCATTTTCGAGCGCCACCGCGGCGGCGGCG 180
QY 181 ACGCCCCCGGGGCTGCGAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
DB 181 ACGCCCCCGGGGCTGCGAGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 240
QY 241 TGAGCCCCCGGCGCGCGGAACTTGGCGGCGACCGCGGCGGCGGCGGCGGCGGCG 300
DB 241 TGAGCCCCCGGCGCGCGGAACTTGGCGGCGACCGCGGCGGCGGCGGCGGCGGCG 300
QY 301 CTCCCCCGCGCGCGCTCTGATCGGGGCGCCAGCTCCGGGCGCGCGGCGGCGGCGG 360
DB 301 CTCCCCCGCGCGCGCTCTGATCGGGGCGCCAGCTCCGGGCGCGCGGCGGCGGCGG 360
QY 361 CCGCGGCG 420
DB 361 CCGCGGCG 420
QY 421 CTTGATGGGGGTCAAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
DB 421 CTTGATGGGGGTCAAGACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480
QY 481 GTGCAACTGCAACCGCTTTTGTTCAGAGCATGAGATCAGCGAGCTGGAGTTGTTCA 540
DB 481 GTGCAACTGCAACCGCTTTTGTTCAGAGCATGAGATCAGCGAGCTGGAGTTGTTCA 540
QY 541 GATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
DB 541 GATCATCATCATGCTGCTGATGATGATGATGATGATGATGATGATGATGATGATG 600
QY 601 CCACCTAAGCTGTCTGCAAGCTCTTTCATAGCGCGGCGACAGCGGCGGCGGAGAGA 660
DB 601 CCACCTAAGCTGTCTGCAAGCTCTTTCATAGCGCGGCGACAGCGGCGGCGGAGAGA 660
QY 661 AGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGAGCACAGTGTGAGCAACGG 720
DB 661 AGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGAGCACAGTGTGAGCAACGG 720

QY 721 AATCCAGAGCGGAGGTCTTACGCCCCGCGCTCGGCCACCGACCGGCTGCGCCGTGCGGCC 780
DB 721 AATCCAGAGCGGAGGTCTTACGCCCCGCGCTCGGCCACCGACCGGCTGCGCCGTGCGGCC 780
QY 781 CTTGCGCCAGCGGAGCGGCTTCCACCGCTTCCAGCGCCACCTATCCCTACTGACAGACGA 840
DB 781 CTTGCGCCAGCGGAGCGGCTTCCACCGCTTCCAGCGCCACCTATCCCTACTGACAGACGA 840
QY 841 GATCGACCTGCGCACCCACCATCTTCGCTGTCAAGCGGAGGAGCGCCACCTTACCAGG 900
DB 841 GATCGACCTGCGCACCCACCATCTTCGCTGTCAAGCGGAGGAGCGCCACCTTACCAGG 900
QY 901 CCCTTCGACCTTCAGCTTCGGGACCCCGAGCAGCAGTGTGAACTGAAACCGGAGTCGCT 960
DB 901 CCCTTCGACCTTCAGCTTCGGGACCCCGAGCAGCAGTGTGAACTGAAACCGGAGTCGCT 960
QY 961 GCGCGCACCCCGCAAAACAGAACCATCTTTCGACAGTGTGATGATGATGATGATGATGAT 1020
DB 961 GCGCGCACCCCGCAAAACAGAACCATCTTTCGACAGTGTGATGATGATGATGATGATGAT 1020
QY 1021 CGGCCCCCTGCCCCCGCAGCAGTAACCTCGGGCATCAGCGCCACCTGCTACGGCAGGCGG 1080
DB 1021 CGGCCCCCTGCCCCCGCAGCAGTAACCTCGGGCATCAGCGCCACCTGCTACGGCAGGCGG 1080
QY 1081 GCGCATGAGGAGGCGCGCGCCACCTTACAGCGAGGTCATCGGCCCATACCCGGGTCCTC 1140
DB 1081 GCGCATGAGGAGGCGCGCGCCACCTTACAGCGAGGTCATCGGCCCATACCCGGGTCCTC 1140
QY 1141 CTTCCAGCACCGAGCAGTGGCGCGCTTCTTCTGAGGAGGACCCCGGCTCCACCA 1200
DB 1141 CTTCCAGCACCGAGCAGTGGCGCGCTTCTTCTGAGGAGGACCCCGGCTCCACCA 1200
QY 1201 CACACATCGCGCGCCCTAGAGAGCGAGCCATCTGAGAGCAAGAGAGGATAAACAGAA 1260
DB 1201 CACACATCGCGCGCCCTAGAGAGCGAGCCATCTGAGAGCAAGAGAGGATAAACAGAA 1260
QY 1261 AGGACACCTCTCTAGGGTCCCGCGGCGCGGCTGCGGCTGCGTAGGTGAAAGGCA 1320
DB 1261 AGGACACCTCTCTAGGGTCCCGCGGCGCGGCTGCGGCTGCGTAGGTGAAAGGCA 1320
QY 1321 G 1321
DB 1321 G 1321

RESULT 2
ACN40804
ID ACN40804 standard; cDNA; 4911 BP.
XX ACN40804;
XX ACN40804;
DT 18-NOV-2004 (first entry)
XX Tumour-associated antigenic target (TAT) | cDNA DNA326860, SEQ ID NO:5823.
DE Tumour-associated antigenic target; TAT; human; overexpression; cancer;
KW tumour; diagnosis; cell proliferative disorder; breast cancer;
KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;
KW central nervous system cancer; bladder cancer; pancreatic cancer;
KW cervical cancer; melanoma; leukaemia; hybridisation probe;
KW chromosome identification; chromosome mapping; gene mapping;
XX gene therapy; cytostatic; gene; ss.
OS Homo sapiens.
XX
PN WO2004030615-A2.
XX
PD 15-APR-2004.
XX
PF 29-SEP-2003; 2003WO-US028547.
XX
PR 02-OCT-2002; 2002US-0414971P.
XX

PA (GETH) GENENTECH INC.
 XX Wu TD, Zhang Z, Zhou Y;
 XX MPI; 2004-347921/32.
 XX New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 XX Claim 1; SEQ ID NO 5823; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention
 XX
 SQ Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;

Query Match 98.5%; Score 1301; DB 13; Length 4911;
 Best Local Similarity 100.0%; Pred. No. 3.3e-195;
 Matches 1301; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 AACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGGCGGCGGCGGCGGAG 80
 DB 1 AACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGGCGGCGGCGGCGGAG 60
 QY 81 GCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCGCGGCGGCGGCGGCGG 140
 DB 61 GCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCGCGGCGGCGGCGGCGG 120
 QY 141 TGCAGCGCCATTTTCGAGCGCCACCGCGGCGACTGCGGAGCGCCCGCGGCGGCGG 200
 DB 121 TGCAGCGCCATTTTCGAGCGCCACCGCGGCGACTGCGGAGCGCCCGCGGCGGCGG 180
 QY 201 GGGAGCGCGGGGGGCGGCGGAGCGCGTCCGCGGCACTGAGCGCCCGGCGGCGGCGG 260
 DB 181 GGGAGCGCGGGGGGCGGCGGAGCGCGTCCGCGGCACTGAGCGCCCGGCGGCGGCGG 240
 QY 261 GAACCTTGGGCGGCAACCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 320
 DB 241 GAACCTTGGGCGGCAACCGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
 QY 321 TGCATGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 380
 DB 301 TGCATGCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
 QY 381 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 440
 DB 361 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
 QY 441 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 500
 DB 421 CCGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 QY 501 TGTTCAGAGCATGGAGATCAACGAGCTGGAGTTTGTTCAGATCATCATCTGTTGGTGG 560

Db 481 TGTTCAGAGCATGGAGATCAACGAGCTGGAGTTTGTTCAGATCATCATCTGTTGGTGG 540
 QY 561 TGTTCAGAGCATGGAGATCAACGAGCTGGAGTTTGTTCAGATCATCATCTGTTGGTGG 620
 DB 541 TGTTCAGAGCATGGAGATCAACGAGCTGGAGTTTGTTCAGATCATCATCTGTTGGTGG 600
 QY 621 GGTTCCTTCATCAGCCGCGCAGCAGCGGCGGAGGAGAGATGATGCTCTCTCAGAG 680
 DB 601 GGTTCCTTCATCAGCCGCGCAGCAGCGGCGGAGGAGAGATGATGCTCTCTCAGAG 660
 QY 681 GATGCGCTGTGGCCCTCGGAGAGCAGATGTTCAGGCAACGAATCCAGAGCGCGAGTCT 740
 DB 661 GATGCGCTGTGGCCCTCGGAGAGCAGATGTTCAGGCAACGAATCCAGAGCGCGAGTCT 720
 QY 741 ACGCCCGCGCTCGGCCCGCACCGAGCTGGCGCTGGCGCTTCGCCCGAGCGGAGCGCT 800
 DB 721 ACGCCCGCGCTCGGCCCGCACCGAGCTGGCGCTGGCGCTTCGCCCGAGCGGAGCGCT 780
 QY 801 TCACCGCTTCAGCGCCACCTATTCCTGATCTTCGAGCAGAGATCGACCTCCACCA 860
 DB 781 TCACCGCTTCAGCGCCACCTATTCCTGATCTTCGAGCAGAGATCGACCTCCACCA 840
 QY 861 TCTCGCTGTACAGCGGAGGAGCGCCCGCCTACCGAGGCGCGCTGCACCTCCAGCTTC 920
 DB 841 TCTCGCTGTACAGCGGAGGAGCGCCCGCCTACCGAGGCGCGCTGCACCTCCAGCTTC 900
 QY 921 GGGACCCCGAGCAGAGCTGGAACCTGAAACCGGAGTGGTGCAGCGCACCCCGCAACAGAA 980
 DB 901 GGGACCCCGAGCAGAGCTGGAACCTGAAACCGGAGTGGTGCAGCGCACCCCGCAACAGAA 960
 QY 981 CCATCTTCAGAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1040
 DB 961 CCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1020
 QY 1041 GTAACTTCGGGCGATCAGCGGCGCATGCTACGGGAGCGGCGGCGGCGGCGGCGGCGGCGG 1100
 DB 1021 GTAACTTCGGGCGATCAGCGGCGCATGCTACGGGAGCGGCGGCGGCGGCGGCGGCGGCGG 1080
 QY 1101 CCACCTTACAGCGAGGCTCATCGGCGCATACCGGCGGCTCTCTTCCAGCAGCAGCAGCAGCA 1160
 DB 1081 CCACCTTACAGCGAGGCTCATCGGCGCATACCGGCGGCTCTCTTCCAGCAGCAGCAGCAGCA 1140
 QY 1161 GTGGGCGGCGCTCTTGTGGAGGAGCGCGGCTCCACACACACACACATCGCGCGGCTAG 1220
 DB 1141 GTGGGCGGCGCTCTTGTGGAGGAGCGCGGCTCCACACACACACATCGCGCGGCTAG 1200
 QY 1221 AGAGCGGCGGCGCTCTTGTGGAGGAGCGCGGCTCCACACACACACATCGCGCGGCTAG 1280
 DB 1201 AGAGCGGCGGCGCTCTTGTGGAGGAGCGCGGCTCCACACACACACATCGCGCGGCTAG 1260
 QY 1281 CCAGCGGCGGCGGCGGCTGGGCGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1321
 DB 1261 CCAGCGGCGGCGGCGGCTGGGCGTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGG 1301

RESULT 3
 ACC49552
 ID ACC49552 standard; cDNA; 4839 BP.
 XX ACC49552;
 AC
 XX
 XX 01-JUL-2003 (first entry)
 XX
 DE Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.
 XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
 KW cancer; gene; ss.
 XX Homo sapiens.
 OS
 XX
 FN WO2003024392-A2.
 XX

XX AC	ADP65729;	Db	1	GGAAAGCTAGCGGACAGAGGCTCAGCCCCCGCGGAGCGCGGCGCCCGCTGCGCCGCTGCGACGCCAATT	60
XX DT	12-AUG-2004 (first entry)	QY	153	TTCCGAGACGCCACCCCGCGGCGCACTGCGGAGCGCCCGCGGGGCTGCCGAGGGAGGCGCGGG	212
XX DE	Human transmembrane, prostate androgen induced RNA (TMPEPAI), DNA.	Db	61	TTCCGAGACGCCACCCCGCGGCGCACTGCGGAGCGCCCGCGGGTGCAGAGGGAGGCGCGGG	120
XX KW	autoimmune disease; arthritis; gene expression analysis;	QY	213	GGGCGAGCGGAGCGCGGTCCTCGCGCACTGAGCCCCCGCGGCGCCCGGGAACTTGGCGGC	272
XX KW	rheumatoid arthritis; collagen-induced; immunosuppressive; antirheumatic;	Db	121	GGGCGAGCGGAGCGCGGTCCTCGCGCACTGAGCCCCCGCGGCGCCCGGGAACTTGGCGGC	180
XX KW	antiarthritic; osteopathic; antigout; antinflammatory; dermatological;	QY	273	GGCCCCAGCCCCGCGGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTCTCGCATGCCGGGC	332
XX KW	immunomodulatory; lupus; ankylosing spondylitis; Fibrositis;	Db	181	GACCCGAGCCCCGCGGAGCGCGGCGCGCTCCCGCGCGCGCGCTCTCGCATGCCGGGC	240
XX KW	fibromyalgia; osteoarthritis; gout; juvenile rheumatoid arthritis;	QY	333	CCGAGCTCCGCGGCGCGCGGAGCGCGCCCGCGGCGCCCGCGAGCCCCCGCGCGCCCGC	392
XX OS	Homo sapiens.	Db	241	CCGAGCTCCGCGGCGCGCGGAGCGCGCCCGCGGCGCCCGCGAGCCCCCGCGCGCCCGC	300
XX PN	W02003072827-A1.	QY	393	GCGCGCGCGCGCGCGCTCCATGCAACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCG	452
XX PD	04-SEP-2003.	Db	301	GCGCGCGCGCGCGCGCTCCATGCAACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCG	360
XX PF	31-OCT-2002; 2002WO-US035433.	QY	453	CGCGCGGCGAGCCCCCATGTCTCTGCACTGCACTGCAAACTGCTTTGTTCCAGAGCA	512
XX PR	31-OCT-2001; 2001US-0336220P.	Db	361	CGCGCGGCGAGCCCCCATGTCTCTGCACTGCACTGCAAACTGCTTTGTTCCAGAGCA	420
XX PA	(CHIL-) CHILDREN'S HOSPITAL MEDICAL CENT.	QY	513	TGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGATGA	572
XX PI	Hirsch R, Thorton SL;	Db	421	TGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGATGA	480
XX PP	WPI: 2003-712740/57.	QY	573	TGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGATGA	632
XX DR	GENBANK; NM_020182.	Db	481	TGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGATGATGATGA	540
XX DR	Diagnosing and analyzing autoimmune disease using gene expression	QY	633	GCGCGCACAGCGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	692
XX PT	profiles and microarray technology, useful for diagnosing and treating	Db	541	GCGCGCACAGCGGCGGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	600
XX PT	rheumatoid arthritis, lupus, fibrositis, osteoarthritis, fibromyalgia and	QY	693	CCTCGGAGAGCAGAGTGTGAGCAACGGAATCCAGAGCGGAGGTCTACGCGCCCGCTC	752
XX PT	gout.	Db	601	CCTCGGAGAGCAGAGTGTGAGCAACGGAATCCAGAGCGGAGGTCTACGCGCCCGCTC	660
XX PS	Disclosure; Page; 56pp; English.	QY	753	GGCCACCGAGCGCGCTGCGCGCTTTCGCGCGGAGCGCGCTTTCGCGCGGAGCGCGCTT	812
XX CC	The invention relates to a novel method for diagnosing and analysing	Db	661	GGCCACCGAGCGCGCTGCGCGCTTTCGCGCGGAGCGCGCTTTCGCGCGGAGCGCGCTT	720
XX CC	autoimmune disease or arthritis. The method comprises obtaining a	QY	813	AGCCACCTATCCGTACCTGCGAGCAGAGTGCAGCTGCGAGCGAGTGCAGCTGCGAGC	872
XX CC	patient sample containing mRNA, analysing gene expression using the mRNA	Db	721	AGCCACCTATCCGTACCTGCGAGCAGAGTGCAGCTGCGAGCGAGTGCAGCTGCGAGC	780
XX CC	that results in a gene expression signature of the mRNA, and using that	QY	873	ACGGGAGGAGCGCCCGACCCCTACCGGGGCGCTGCGAGCGCGCTTTCGCGGAGCGCGG	932
XX CC	gene expression signature to diagnose or analyse the autoimmune disease	Db	781	ACGGGAGGAGCGCCCGACCCCTACCGGGGCGCTGCGAGCGCGCTTTCGCGGAGCGCGG	840
XX CC	or arthritis in the patient, where gene expression of at least 60% of	QY	933	AGCAGCTGGAATGGAACCGGGAGTGGTGGCGCGACCCCTGCGAGCGCGCTTTCGCGGAG	992
XX CC	the genes correlates with that of the gene signature. The invention	Db	841	AGCAGCTGGAATGGAACCGGGAGTGGTGGCGCGACCCCTGCGAGCGCGCTTTCGCGGAG	900
XX CC	further comprises: a treatment of rheumatoid arthritis; identification of	QY	993	GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	1052
XX CC	genes for targeting in the treatment of rheumatoid arthritis in a mammal	Db	901	GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG	960
XX CC	other than a mouse, diagnosis of rheumatoid arthritis in a mammal, an	QY	1053	TCAGCGCCACGTGCTACCGGCGCGGCGCGATGAGGAGGCGCGCGCGCGCGCGCGCGCG	1112
XX CC	array or gene chip, specific for rheumatoid arthritis; diagnosis or	Db	961	TCAGCGCCACGTGCTACCGGCGCGGCGCGATGAGGAGGCGCGCGCGCGCGCGCGCGCG	1020
XX CC	analyses of autoimmune disease or rheumatoid arthritis; screening the	QY	1113	AGGTATGCGGCGCACTACCGGCGGCTCTCTTTCAGGCAACAGGAGAGAGAGAGAGAGAG	1172
XX CC	efficacy of a candidate drug in vitro for the treatment of collagen-	Db	1021	AGGTATGCGGCGCACTACCGGCGGCTCTCTTTCAGGCAACAGGAGAGAGAGAGAGAGAG	1080
XX CC	induced arthritis; and reducing the symptoms associated with collagen-	QY	1173	CCTTCTGAGGAGGAGCGCGGCTTCCACCAACACACATCGCGCGCGCTTAGAGAGCGGCA	1232
XX CC	induced arthritis. The compositions of the invention have the following	Db	1081	CCTTCTGAGGAGGAGCGCGGCTTCCACCAACACACATCGCGCGCGCTTAGAGAGCGGCA	1140
XX CC	activities: immunosuppressive, antirheumatic, antiarthritic, osteopathic,				
XX CC	antigout, antinflammatory, dermatological, and immunomodulatory. The				
XX CC	methods and compositions of the present invention are useful for				
XX CC	diagnosing and treating autoimmune disease or arthritis, such as				
XX CC	rheumatoid arthritis, lupus, ankylosing spondylitis, fibrositis,				
XX CC	immune disease caused by an infectious agent. This polynucleotide				
XX CC	represents a DNA sequence relating to the genes used in the analysis and				
XX CC	treatment of autoimmune diseases or arthritis. Note: This sequence is				
XX CC	not shown in the specification. It has been supplied in an electronic				
XX CC	format from WIPO.				
XX SQ	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;				
XX	Query Match 93.0%; Score 1229; DB 11; Length 4839;				
XX	Best Local Similarity 100.0%; Pred. No. 6.4e-184;				
XX	Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
XX	QY 93 GGAAAGCTAGCGGAGGCTCAGCCCCCGCGGAGCGCGGCGCCCGCTGCGCCGCTGCGACGCCAATT				152

Qy	1233	TCTGGACCAAGAGAGATTAACAGAAAAGGACACCTCTCTCTAGGGTCCCAAGGGGGGCC	1239
Db	1141	TCTGGACCAAGAGAGAGATTAACAGAAAAGGACACCTCTCTCTAGGGTCCCAAGGGGGGCC	1200
Qy	1293	GGGCTGGGGTGGCTAGGTGAAAAGGCAG	1321
Db	1201	GGGCTGGGGTGGCTAGGTGAAAAGGCAG	1229
RESULT 6			
ADM67045			
ID	ADM67045	standard; DNA; 4839 BP.	
XX	ADM67045;		
XX	03-JUN-2004	(first entry)	
XX		Human homologue of murine adipocyte specific DNA SeqID 180.	
DE			
XX		human; adipocyte specific; ds; adipose tissue; anti-obesity;	
KW		high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;	
KW		adipogenesis; hypertension; cardiovascular disease; anorectic;	
KW		antidiabetic; hypotensive.	
XX			
OS		Homo sapiens.	
XX			
PN	W02004011618-A2.		
XX			
PD	05-FEB-2004.		
XX			
PF	29-JUL-2003; 2003WO-US023684.		
XX			
PR	29-JUL-2002; 2002US-0398785P.		
PR	12-JUN-2003; 2003US-0478206P.		
XX			
PA	(HMGE-) HMGENE INC.		
XX			
PI	Chada K, Chouinard R, Ashar H, Sayed AMD;		
DR	WPI; 2004-143846/14.		
XX			
PT	Identifying adipocyte specific genes, useful for treating obesity or		
PT	diabetes, and for identifying drug targets, by differential gene		
PT	expression analysis between adipose tissue or stromal vascular tissue of		
PT	mouse of different genotypes.		
XX			
PS	Claim 11; SEQ ID NO 180; 91pp; English.		
XX			
CC	This invention relates to a novel method for identifying genes that are		
CC	over-expressed in adipose tissue and as such it provides targets for anti		
CC	-obesity pharmaceutical compositions. Specifically, it refers to a high		
CC	mobility group I-C protein (HMGI-C) that is associated with obesity and		
CC	is epistatic to leptin, furthermore, it refers to the ob gene where an		
CC	autosomal recessive trait is linked to obesity and diabetes. The present		
CC	invention describes performing differential gene expression analysis		
CC	between the white adipose tissue (WAT) or stromal vascular tissue (SVT)		
CC	of any two different mice selected from a group consisting of wild-type,		
CC	HMGI-C -/-, ob/ob, or HMGI-C -/- ob/ob genotype mice. Accordingly, using		
CC	this method novel nucleotides and the encoded proteins thereof were		
CC	identified that are adipocyte specific, and as such can be used for		
CC	preventing adipogenesis, diagnosing and treating diabetes, obesity,		
CC	hypertension and cardiovascular disease, as well as screening for		
CC	compounds that can modulate or prevent adipogenesis and treat diabetes or		
CC	obesity. These compositions exhibit anorectic, antidiabetic and		
CC	hypotensive activities. This polynucleotide sequence is a human homologue		
CC	of a murine adipocyte specific DNA sequence of the invention.		
XX			
SQ	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;		
Query Match		93.0%; Score 1229; DB 12; Length 4839;	
Best Local Similarity	100.0%;	Prod. No. 6.4e-184;	
Matches 1229; Conservative	0; Mismatches	0; Indels	0; Gaps

Db 781 ACGGAGGAGCCGCCACCTACCGGGCCCTGACCTTCAGCTTCGGACCCCGAGC 840
QY 933 AGCAGCTGGAACCTGAACCGGAGTGGTGGCGGCAACCCCAAGAACATCTTCGACA 992
Db 841 AGCAGCTGGAACCTGAACCGGAGTGGTGGCGGCAACCCCAAGAACATCTTCGACA 900
QY 993 GTGACCTGTGATAGTGCAGGCTGGGCGGCCCTGCCCCCAGCAGTACTCGGGCA 1052
Db 901 GTGACCTGTGATAGTGCAGGCTGGGCGGCCCTGCCCCCAGCAGTACTCGGGCA 960
QY 1053 TCAGGCCCACTGCTACTAGCGGAGCGGGCGGCATGAGGGGGCGCGCCCACTACAGCG 1112
Db 961 TCAGGCCCACTGCTACTAGCGGAGCGGGCGGCATGAGGGGGCGCGCCCACTACAGCG 1020
QY 1113 AGGTATCGGCCCACTACCGGGGTCTCTTCAGCACCAGCAGAGCAGTGGCGCCCT 1172
Db 1021 AGGTATCGGCCCACTACCGGGGTCTCTTCAGCACCAGCAGAGCAGTGGCGCCCT 1080
QY 1173 CTTGCTGAGGGGACCGGCTCCACACACACATCGGGCCCTTAGAGGGGAGCCA 1232
Db 1081 CTTGCTGAGGGGACCGGCTCCACACACACATCGGGCCCTTAGAGGGGAGCCA 1140
QY 1233 TCTGAGCAAGAGAGAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCC 1292
Db 1141 TCTGAGCAAGAGAGAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCGAGGGGGCC 1200
QY 1293 GGGCTGGGGCTGCTAGGTGAAAGGAG 1321
Db 1201 GGGCTGGGGCTGCTAGGTGAAAGGAG 1229

RESULT 8

ADR66778
ID ADR66778 standard; DNA; 4839 BP.

AC ADR66778;

DT 02-DEC-2004 (first entry)

DE Human prostatic carcinoma derived DNA SEQ ID 71 #4.

KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; ds.

OS Homo sapiens.

PN WO2004076614-A2.

PD 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DE000433.

XX 27-FEB-2003; 2003DE-01009985.

PR 14-MAY-2003; 2003DE-01022134.

XX

PA (HINZ/) HINZMANN B.

PA (DAHL/) DAHL E.

PA (ROSE/) ROSENTHAL A.

PA (HERM/) HERMANN K.

PA (PILA/) PILARSKY C.

XX

PI Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;

PI Schmitt A, Beckmann G, Bruemmendorf T, Kinnemann H, Roepcke S;

PI Xinzhong L, Staub E;

XX WPI; 2004-653386/63.

DR New nucleic acids, and encoded proteins, from prostatic cancer tissue,

PT useful for diagnosis, treatment and in screening for specific binding

PT agents.

XX Claim 1; Page 1447; 1607pp; German.

PS

XX

CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotope. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC CD24 was upregulated in many of them. Sections of tissue, isolated from
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then dianinobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.
XX

SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 13; Length 4839;
Best Local Similarity 100.0%; Pred. No. 6.4e-184;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGCAGAGCTCAGCCCCCGCGGCGCAGCGCGCGCCGCGCCATT 152
Db 1 GGAAGCTAGCGCAGAGCTCAGCCCCCGCGGCGCAGCGCGCGCCGCGCCATT 60
QY 153 TTCGGAGCCACCCCGGGGCACTGCGGAGCCCCCGGGGCTGCCGAGGGGCGGGG 212
Db 61 TTCGGAGCCACCCCGGGGCACTGCGGAGCCCCCGGGGCTGCCGAGGGGCGGGG 120
QY 213 GGGCGCAGCGAGCGCGGTCCCGCAGCTGAGCCCCCGCGGCGCCCGGAACTTGGCGC 272
Db 121 GGGCGCAGCGAGCGCGGTCCCGCAGCTGAGCCCCCGCGGCGCCCGGAACTTGGCGC 180
QY 273 GACCCGAGCCCGCGAGCGGGGCGCGCTTCCCGCGCGCGCGCGCTTCTGCAATGCGGGC 332
Db 181 GACCCGAGCCCGCGAGCGGGGCGCGCTTCCCGCGCGCGCGCGCTTCTGCAATGCGGGC 240
QY 333 CCGAGCTCCGGGCGCGCGGAGCCCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 392
Db 241 CCGAGCTCCGGGCGCGCGGAGCCCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 300
QY 393 GCGGCGCGCGCGCGCTCCATGCACTGATGGGGGTCAACAGCACCGCGCGCGCGCG 452
Db 301 GCGGCGCGCGCGCGCTCCATGCACTGATGGGGGTCAACAGCACCGCGCGCGCGCGCG 360
QY 453 CCG 512
Db 361 CCG 420
QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGA 572
Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGA 480
QY 573 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 632
Db 481 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540

QY 713 GGCAACGGAATCCAGAGCGCGAGGTCTACGCCCGCTCGGCCCAACCGACCGCTGGCC 772
 Db 301 GGCAACGGAATCCAGAGCGCGAGGTCTACGCCCGCTCGGCCCAACCGACCGCTGGCC 360
 QY 773 GTGCGCGCTTCGCCCGAGCGGAGCGCTTCACGGCTTCAGCGCCACCTATCCGTACTG 832
 Db 361 GTGCGCGCTTCGCCCGAGCGGAGCGCTTCACGGCTTCAGCGCCACCTATCCGTACTG 420
 QY 833 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTCAGACGGGAGAGCCGCCACCC 892
 Db 421 CAGCAGAGATCGACCTGCGCACCCACCATCTCGCTGTCAGACGGGAGAGCCGCCACCC 480
 QY 893 TACCAGGGCCCTTCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCTGAAACCGG 952
 Db 481 TACCAGGGCCCTTCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCTGAAACCGG 540
 QY 953 GAGTCGGTGGCGGACCCCAACAGAACCATCTTCGACAGTCAGTACCTGATGATGTC 1012
 Db 541 GAGTCGGTGGCGGACCCCAACAGAACCATCTTCGACAGTCAGTACCTGATGATGTC 600
 QY 1013 AGGCTGGGGCGCCCTGCGCCCCCGCCAGCAGTAACCTCGGGCATCAGCGCAGCTGCTACGGC 1072
 Db 601 AGGCTGGGGCGCCCTGCGCCCCCGCCAGCAGTAACCTCGGGCATCAGCGCAGCTGCTACGGC 660
 QY 1073 AGCGGGCGCGCATGGAGGGCGCGCCGCCACCTACAGCGAGGTCTATCGGCCCACTACCGG 1132
 Db 661 AGCGGGCGCGCATGGAGGGCGCGCGCCGCCACCTACAGCGAGGTCTATCGGCCCACTACCGG 720
 QY 1133 GGGTCTCTCTTCAGCAGCAGCAGAGCAGTGGCGCGCCCTCTCTGTCGAGGGGACCGG 1192
 Db 721 GGGTCTCTCTTCAGCAGCAGCAGAGCAGTGGCGCGCCCTCTCTGTCGAGGGGACCGG 780
 QY 1193 CTCACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 1252
 Db 781 CTCACACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAGGAT 840
 QY 1253 AAACAGAAAGGACACCTCTCTTAG 1276
 Db 841 AAACAGAAAGGACACCTCTCTTAG 864

RESULT 11
 AAA75151
 ID AAA75151 standard; cDNA; 969 BP.
 XX
 AC AAA75151,
 XX
 DT 15-JAN-2001 (first entry)
 DE
 XX cDNA encoding a human TANGO 261 polypeptide.
 XX
 KW TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267;
 KW cellular proliferation; cellular differentiation; cellular adhesion;
 KW von Willebrand factor-associated disorder; cell trafficking; cancer;
 KW hematopoietic associated disease; atelectasis; pulmonary congestion;
 KW oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis;
 KW intestinal disorder; spleen associated disease; renal disorder;
 KW cardiovascular disorder; ischemic heart disease; hydrocephalus;
 KW brain herniation; iatrogenic disease; inflammation; meningitis;
 KW Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease;
 KW multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder; ss.
 XX
 OS Homo sapiens.
 XX
 XX
 PH Key Location/Qualifiers
 FT CDS 6..764
 FT /*tag= a
 FT /product= "TANGO 261"
 FT sig_peptide 6..89
 FT /*tag= b
 FT mat_peptide 90..764
 FT /*tag= c

XX WO200052022-A1.
 PN
 PD 08-SEP-2000.
 XX
 PF 01-MAR-2000; 2000WO-US005226.
 XX
 PR 01-MAR-1999; 99US-0122458P.
 XX
 PA (MILL-) MILLENNIUM PHARM INC.
 XX
 PI Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
 XX
 DR WPI; 2000-579269/54.
 DR P-PSDB; AAB18449.
 XX
 PT Novel human and murine secreted proteins designated TANGO 216, 261, 262,
 PT 266 and 267 useful as modulating agents of cellular processes, e.g. for
 PT treating cancer.
 XX
 PS Claim 2; Fig 5; 175pp; English.
 CC
 CC The present sequence encodes a human TANGO 261 polypeptide. The
 CC specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
 CC 267. The TANGO polypeptides can be used to modulate cellular
 CC proliferation, modulate cellular differentiation and/or modulate cellular
 CC adhesion. The proteins can be used to treat any von Willebrand factor-
 CC associated disorder, regulate extracellular matrix structuring, cellular
 CC adhesion, and cell trafficking and/or migration, modulate cellular
 CC interactions, modulate cell adhesion in proliferative disorders, such as
 CC cancer, modulate the proliferation, differentiation, and/or function of
 CC cells that appear in the bone marrow, and leukocytes, treat bone marrow,
 CC blood and hematopoietic associated diseases and disorders, atelectasis,
 CC pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
 CC asthma and bronchiectasis, intestinal disorders, spleen associated
 CC diseases, modulate renal disorders, treat cardiovascular disorders such
 CC as ischemic heart disease, modulate the proliferation, differentiation,
 CC and/or function of bone and cartilage cells and to treat bone and/or
 CC cartilage associated diseases or disorder. They may also be used to treat
 CC disorders associated with the ovaries, cerebral oedema, hydrocephalus,
 CC brain herniations, iatrogenic disease, inflammations, bacterial and viral
 CC meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
 CC disease, multiple sclerosis, brain cancers, hydrocephalus and
 CC encephalitis, and treat hepatic disorders
 XX
 SX Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;
 QY
 Db 514 GGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGATGATGATGAT 573
 Db 2 GGAGATGCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGATGATGATGATGAT 61
 QY 574 GGTGGTGGTGATCAGCTGCTCTGAGCCATACAGCTGTCTGCACGGTCTCTCATCAG 633
 Db 62 GGTGGTGGTGATCAGCTGCTCTGAGCCATACAGCTGTCTGCACGGTCTCTCATCAG 121
 QY 634 CCGGACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCC 693
 Db 122 CCGGACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCC 181
 QY 694 CTCGGAGACAGTGTTCAGCAACGGATCCAGAGCGCAGGTTACGCCCGCTCG 753
 Db 182 CTCGGAGACAGTGTTCAGCAACGGATCCAGAGCGCAGGTTACGCCCGCTCG 241
 QY 754 GCCCACCGACCGCTGGCGCTGCGCCCTTCCGCCAGCGGGAGCGCTTCCACCGTTCCA 813
 Db 242 GCCCACCGACCGCTGGCGCTGCGCCCTTCCGCCAGCGGGAGCGCTTCCACCGTTCCA 301
 QY 814 GCCCACCTATCCGTACCTGTCAGCAGATGACCTGCCACCCACCATCTCGTGTCCA 873

Query Match 60.8%; Score 803.2; DB 3; Length 969;
 Best Local Similarity 99.6%; Pred. No. 3.8e-117;
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Db 302 GCCACCTATCGTACCTGACGACGAGATCGACCTGCGGCCCAACCATCTCGTGTGAGA 361
Qy 874 CGGGAG 933
Db 362 CGGGAG 421
Qy 934 GCAGCTGGAAGTGAACCGGAGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 993
Db 422 GCAGCTGGAAGTGAACCGGAGTGGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 481
Qy 994 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1053
Db 482 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
Qy 1054 CAGCGCCACATGCTACGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1113
Db 542 CAGCGCCACATGCTACGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601
Qy 1114 GGTATCGGCGCATACCGGGGTCCTCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 1173
Db 602 GGTATCGGCGCATACCGGGGTCCTCTTCCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 661
Qy 1174 CTTGCTGGAGGGAGCGCGGCTCCACACACACACACACACACACACACACACACACAC 1233
Db 662 CTTGCTGGAGGGAGCGCGGCTCCACACACACACACACACACACACACACACACACAC 721
Qy 1234 CTGGAGCAAGAGAGAGATAAACAGAAAGGACACCTCTCTAGGGTCCCGGAGGAGCGG 1293
Db 722 CTGGAGCAAGAGAGAGATAAACAGAAAGGACACCTCTCTAGGGTCCCGGAGGAGCGG 781
Qy 1294 GGCTGGGCTGCTAGGTGAAAGGCGAG 1321
Db 782 GGCTGGGCTGCTAGGTGAAAGGCGAG 809

RESULT 12

ABK92120
ID ABK92120 standard; DNA; 1140 BP.

XX
AC ABK92120;

DT 15-AUG-2002 (first entry)

XX Prostate cancer-associated DNA sequence #6.

XX Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;

XX gene therapy; gene; ds.

XX Mammalia.

OS WO200230268-A2.

XX 18-APR-2002.

XX 12-OCT-2001; 2001WO-05032045.

XX 13-OCT-2000; 2000US-00687576.

XX 08-DEC-2000; 2000US-00733288.

XX 08-DEC-2000; 2000US-00733742.

XX 24-JAN-2001; 2001US-0263957P.

XX 16-MAR-2001; 2001US-0276791P.

XX 06-APR-2001; 2001US-0281922P.

XX 24-APR-2001; 2001US-0286214P.

XX 30-APR-2001; 2001US-00847046.

XX 04-MAY-2001; 2001US-0288589P.

XX (BOSB-) EOS BIOTECHNOLOGY INC.

XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;

XX WPI; 2002-471335/50.

DR P-PSDB; ABG61805.

XX

PT Detecting a prostate cancer-associated transcript in a cell in a patient,
PT useful for diagnosing prostate cancer (PC) or screening modulators of PC,
PT by determining if prostate cancer-associated genes are expressed in a
PT prostate tissue.

XX Claim 22; Page 305; 436pp; English.

XX The present invention relates to methods of detecting a prostate cancer-
XX associated transcript in a cell from a patient. The method comprises
XX contacting a biological sample from the patient with prostate cancer-
XX associated polynucleotides (designated PC genes) that selectively
XX hybridize to a sequence that is at least 80% identical to them. The
XX prostate cancer-associated polynucleotide sequences are differentially
XX expressed in prostate tumour tissue or in prostate cancer and are derived
XX from the tissues of various organisms such as humans or other mammals
XX (e.g. mice, sheep and dogs). The methods of the invention are useful for
XX diagnosing and treating prostate cancer in mammals. The prostate cancer-
XX associated genes are useful for diagnosing or treating prostate cancer,
XX as well as for identifying modulators of prostate cancer or agents that
XX inhibit prostate cancer. The nucleic acid sequences are particularly
XX useful in gene therapy, as a vaccine or in antisense applications.
XX ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
XX sequences

XX Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match 60.7%; Score 802.2; DB 6; Length 1140;

Best Local Similarity 98.4%; Pred. No. 5.4e-117;

Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

Qy 499 TTTGTTCCAGAGCATCGAGATCACGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGT 558

Db 77 TCTCTCGCAAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGT 136

Qy 559 GGTGATGATGTTGATGGTGGTGTGATCAGTCCCTGCTGAGCCACTACAGCTGTCTGC 618

Db 137 GGTGATGATGTTGATGGTGGTGTGATCAGTCCCTGCTGAGCCACTACAGCTGTCTGC 196

Qy 619 ACGTCTCTTCATCAGCGCGGCACAGCCAGGGCGGAGAGAGAGAGATGCTCTCTCAGA 678

Db 197 ACGTCTCTTCATCAGCGCGGCACAGCCAGGGCGGAGAGAGAGATGCTCTCTCAGA 256

Qy 679 AGGATGCTGTGGCCCTTCGAGAGAGCAAGTGTGAGCAACGGAATCCAGAGCGCAGGT 738

Db 257 AGGATGCTGTGGCCCTTCGAGAGAGCAAGTGTGAGCAACGGAATCCAGAGCGCAGGT 316

Qy 739 CTAGCGCCCGCTTCGGGCCACCGACCGCTGGCGGTGGCCCTTCGCGCCAGCGGAGCG 798

Db 317 CTAGCGCCCGCTTCGGGCCACCGACCGCTGGCGGTGGCCCTTCGCGCCAGCGGAGCG 376

Qy 799 CTTCCACCGCTTCAGCCCACTATCCGTACTGTCAGCAGCAGATCGACCTGCCACCCAC 858

Db 377 CTTCCACCGCTTCAGCCCACTATCCGTACTGTCAGCAGCAGATCGACCTGCCACCCAC 436

Qy 859 CATCTCGTGTACAGCGGGAGAGCCCCACCTACCGAGGCCCTTCGACCTCCAGCT 918

Db 437 CATCTCGTGTACAGCGGGAGAGCCCCACCTACCGAGGCCCTTCGACCTCCAGCT 496

Qy 919 TCGGGACCCCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGGACCCCGCAACAG 978

Db 497 TCGGGACCCCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGGACCCCGCAACAG 556

Qy 979 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1038

Db 557 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616

Qy 1039 CAGTAACTCGGGCATCAGGCCACGCTGCTACGGCAGCGCGGCGCATGAGAGGGCGGCC 1098

Db 617 CAGTAACTCGGGCATCAGGCCACGCTGCTACGGCAGCGCGGCGCATGAGAGGGCGGCC 676

Qy 1099 GCCCACCCTACAGGAGGTGATCGGCCACTTACCCGGGGTCTCTTCTCAGCAGCAGCAGAG 1158

Db 677 GCCCACCTACAGCGAGGTTCATCGGCCACTACCCGGGGTCTCTCCAGCACACGAGAG 736
 QY 1159 CAGTGGGCGGCCCTCTCTGCTGGAGGGACCCGGCTCCACCACACACACATCGCGCCCT 1218
 Db 737 CAGTGGGCGGCCCTCTCTGCTGGAGGGACCCGGCTCCACCACACACACATCGCGCCCT 796
 QY 1219 AGAGAGCGCAGCCATCTGGAGCAAGAGAAAGATTAACAGAAAGACACCCCTCTCTAGGG 1278
 Db 797 AGAGAGCGCAGCCATCTGGAGCAAGAGAAAGATTAACAGAAAGACACCCCTCTCTAGGG 856
 QY 1279 TCCCCAGGGGGCGGGCTGGGGCTGGTAGGTGAAAAGGAG 1321
 Db 857 TCCCCAGGGGGCGGGCTGGGGCTGGTAGGTGAAAAGGAG 899

RESULT 13

ADB75588

ID ADB75588 standard; cDNA; 1141 BP.

XX AC ADB75588;

XX DT 04-DEC-2003 (first entry)

XX DE Prostate cancer marker cDNA.

XX KW Prostate; cancer; cytostatic; gene therapy; marker; ss.

XX OS Homo sapiens.

XX PN WO2003009814-A2.

XX PD 06-FEB-2003.

XX PF 25-JUL-2002; 2002WO-US023913.

XX PR 25-JUL-2001; 2001US-0307982P.

XX PR 22-AUG-2001; 2001US-0314356P.

XX PR 25-SEP-2001; 2001US-0325020P.

XX PR 12-DEC-2001; 2001US-0341746P.

XX PR 05-MAR-2002; 2002US-0362158P.

XX PA (MILL-) MILLENNIUM PHARM INC.

XX PI Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;
 XX PI Hoerhn S, Kamatkar S, Monsey AM, Glatt K, Zhao X, Anderson D;
 XX PI WPI; 2003-248033/24.

XX PT New nucleic acid molecule, useful for diagnosing or treating prostate
 XX PT cancer.

XX PS Disclosure; SEQ ID NO 412; 99pp; English.

XX CC The invention relates to newly discovered cancer markers associated with
 CC CC the cancerous state of prostate cells. Also disclosed is a method of
 CC CC assessing whether a patient is afflicted with prostate cancer. The method
 CC CC of the invention involves assessing whether a patient is afflicted with
 CC CC prostate cancer by comparing the level of expression of a marker in a
 CC CC patient sample and the normal level of expression of the marker in a
 CC CC control non-prostate cancer sample, where a significant increase in the
 CC CC level of expression of the marker in the patient sample and the normal
 CC CC level indicates that the patient is afflicted with prostate cancer.
 CC CC Nucleic acids of the invention are useful for diagnosing or treating
 CC CC prostate cancer, and may be useful in gene therapy. Sequences given in
 CC CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence
 CC CC data for this patent did not form part of the printed specification, but
 CC CC was obtained in electronic format directly from WIPO at
 CC CC ftp.wipo.int/pub/published_pct_sequences.

SQ Sequence 1141 BP; 271 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match

Best Local Similarity 60.7%; Score 802.2; DB 10; Length 1141;

98.4%; Pred. No. 5.4e-117;

Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
 QY 499 TTGTTCAGAGATCGAGATCAAGAGTGGAGTTTGTTCAGATCATCATCATCTGTGT 558
 Db 77 TCTCTCGCAAAACAGGCAATGGCGAGTGGAGTTTGTTCAGATCATCATCATCTGTGT 136
 QY 559 GGTGATGATGTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
 Db 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
 QY 619 ACGTCTCTTCATCAGCGGCACAGCCAGGGGGGAGAGAGAGATGCTCTCTCTCAGA 678
 Db 197 ACGTCTCTTCATCAGCGGCACAGCCAGGGGGGAGAGAGAGATGCTCTCTCTCAGA 256
 QY 679 AGGATGCTCTGTGGCCCTCGGAGAGCAAGTGTTCAGGCAACGGGAATCCAGAGCGGAGGT 738
 Db 257 AGGATGCTCTGTGGCCCTCGGAGAGCAAGTGTTCAGGCAACGGGAATCCAGAGCGGAGGT 316
 QY 739 CTACGCCCCCGCTCGGCCACACCGCTGCGTGGCGCCCTTCGCGCCAGCGGAGCG 798
 Db 317 CTACGCCCCCGCTCGGCCACACCGCTGCGTGGCGCCCTTCGCGCCAGCGGAGCG 376
 QY 799 CTTTCCACCGCTTCAGGCCACCTATCCGTAACCTGAGCAGCAGATGACCTGCCACCCAC 858
 Db 377 CTTTCCACCGCTTCAGGCCACCTATCCGTAACCTGAGCAGCAGATGACCTGCCACCCAC 436
 QY 859 CATCTCGCTGTGAGAGCGGGGAGGCCCCACCTACCGAGGGCCCTGACCTCCAGCT 918
 Db 437 CATCTCGCTGTGAGAGCGGGGAGGCCCCACCTACCGAGGGCCCTGACCTCCAGCT 496
 QY 919 TCGGGAACCCGAGCAGCAGCTGGAACCTGAACCGGAGTGGTGGCGGACACCCCAACAG 978
 Db 497 TCGGGAACCCGAGCAGCAGCTGGAACCTGAACCGGAGTGGTGGCGGACACCCCAACAG 556
 QY 979 AACCATCTTCGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 1038
 Db 557 AACCATCTTCGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 616
 QY 1039 CAGTAACTCGGGCATCAGCGCCACCTGCTAGGGCAGCGCGGCGCATGGAGGGGCGGCC 1098
 Db 617 CAGTAACTCGGGCATCAGCGCCACCTGCTAGGGCAGCGCGGCGCATGGAGGGGCGGCC 676
 QY 1099 GCCCACTTACAGCAGGTCATCGGCCACTACCCGGGGTCTCTCTTCAGAGCACCAGCAGAG 1158
 Db 677 GCCCACTTACAGCAGGTCATCGGCCACTACCCGGGGTCTCTCTTCAGAGCACCAGCAGAG 736
 QY 1159 CAGTGGGCGGCCCTCTCTGCTGGAGGGACCGGGCTCCACACACACATCGCGCCCT 1218
 Db 737 CAGTGGGCGGCCCTCTCTGCTGGAGGGACCGGGCTCCACACACACATCGCGCCCT 796
 QY 1219 AGAGAGCGCAGCCATCTCGAGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTCTAGGG 1278
 Db 797 AGAGAGCGCAGCCATCTCGAGCAAGAGAGAGATTAACAGAAAGGACACCCCTCTCTAGGG 856
 QY 1279 TCCCCAGGGGGCGGGCTGGGGCTGGTAGGTGAAAAGGAG 1321
 Db 857 TCCCCAGGGGGCGGGCTGGGGCTGGTAGGTGAAAAGGAG 899

RESULT 14

ACC49536

ID ACC49536 standard; cDNA; 1850 BP.

XX AC ACC49536;

XX DT 01-JUL-2003 (first entry)

XX DE Tumour-associated antigenic target protein TAT180 cDNA SEQ ID NO:44.

XX KW Human; tumour-associated antigenic target; TAT; tumour; diagnosis;

XX KW cancer; gene; ss.

XX OS Homo sapiens.

PT treating prostate cancer or other prostatic pathologies, e.g.
PT prostatitis.

XX Claim 9; SEQ ID NO 2; 43pp; English.

XX The invention relates to a substantially pure androgen responsive
CC prostate specific (ARP) nucleic acid molecule selected from ARP1-ARPS
CC (appearing as ADL83312, ADL83313, ADL83315, ADL83317 and ADL83319. Also
CC included are methods of diagnosing or predicting susceptibility to a
CC prostate neoplastic condition in an individual, methods for treating or
CC reducing the severity of a prostate neoplastic condition in an
CC individual, a substantially pure ARP3, ARP4 or ARPS polypeptide (or their
CC fragments, encoded by the above ARP3, ARP4 or ARPS nucleic acid molecule,
CC respectively) and a binding agent comprising a molecule that selectively
CC binds the above ARP3, ARP4 or ARPS polypeptide. The nucleic acid
CC molecules and polypeptides are useful in diagnosing, preventing and
CC treating prostate cancer or other prostate pathologies such as benign
CC prostatic hyperplasia or prostatitis. The nucleic acid molecules are used
CC as hybridisation probes in various diagnostic procedures. The present
CC sequence is the ARP2 cDNA.

XX
SQ Sequence 4527 BP; 1089 A; 1149 C; 1175 G; 1113 T; 0 U; 1 Other;

Query Match 60.7%; Score 802.2; DB 11; Length 4527;
Best Local Similarity 98.4%; Pred. No. 5e-117;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTGTTGTT 558
DB 77 TCTCTCGGAAACAGGCAATGGCGAGCTGGAGTTGTTTCAGATCATCATCTGTTGTT 136
QY 559 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
DB 137 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
QY 619 ACGGTCTTTCATCAGCGGACAGCCAGCGGCGGAGAGAGAGATGCCCTGTCCTCAGA 678
DB 197 ACGGTCTTTCATCAGCGGACAGCCAGCGGCGGAGAGAGATGCCCTGTCCTCAGA 256
QY 679 AGGATGCTGTGGCCCTCGGAGAGCAGTGTGATGATGATGATGATGATGATGATGATGAT 738
DB 257 AGGATGCTGTGGCCCTCGGAGAGCAGTGTGATGATGATGATGATGATGATGATGATGAT 316
QY 739 CTACGGCCCGCCCTCGGCCACCGCCCTGCGCGCCCTGCGCGCCCTGCGCGCGGAGCG 798
DB 317 CTACGGCCCGCCCTCGGCCACCGCCCTGCGCGCCCTGCGCGCCCTGCGCGCGGAGCG 376
QY 799 CTTCCACCGCTTCAGCGGACCTATCGGTACCTGACGACGAGATCGACTGCAACCCAC 858
DB 377 CTTCCACCGCTTCAGCGGACCTATCGGTACCTGACGACGAGATCGACTGCAACCCAC 436
QY 859 CATCTCGCTGTACAGCGGAGAGCGCCCGCCCTACCGGGCCCTGCGCGCCCTGCGCGCT 918
DB 437 CATCTCGCTGTACAGCGGAGAGCGCCCGCCCTACCGGGCCCTGCGCGCCCTGCGCGCT 496
QY 919 TCGGGACCCCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGGACACCCCGCAACAG 978
DB 497 TCGGGACCCCGAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGGACACCCCGCAACAG 556
QY 979 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1038
DB 557 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616
QY 1039 CAGTAACTCGGGATCAGCGGACGCTGCTACGCGAGCGGCGGCGCATGGAGGGCGCC 1098
DB 617 CAGTAACTCGGGATCAGCGGACGCTGCTACGCGAGCGGCGGCGCATGGAGGGCGCC 676
QY 1099 GCCCACTTACAGCGAGGTTCATCGGCCACTACCGGGGTCTCTCTCCAGCAGCAGAG 1158
DB 677 GCCCACTTACAGCGAGGTTCATCGGCCACTACCGGGGTCTCTCTCCAGCAGCAGAG 736
QY 1159 CAGTGGGCGCCCTCTCTGCTGAGGGGACCGGGCTCCACACACATCGCGCCCT 1218

DB 737 CAGTGGGCGCCCTCTCTGCTGAGGGGACCGGGCTCCACACACACATCGCGCCCT 796
QY 1219 AGAGAGCGGAGCCATCTGGAGCAAGAGAGATTAACAGAGGACACCCCTCTCTAGGG 1278
DB 797 AGAGAGCGGAGCCATCTGGAGCAAGAGAGATTAACAGAGGACACCCCTCTCTAGGG 856
QY 1279 TCCCCAGGGGGCGCGGGCTGGGGCTGCGTAGGTGAAAGGCAG 1321
DB 857 TCCCCAGGGGGCGCGGGCTGGGGCTGCGTAGGTGAAAGGCAG 899

Search completed: February 19, 2005, 11:44:04
Job time : 712.116 secs

Db 331 G C C C A C C A C G C C T G C G C C C T T C G C C C A G C G G A G C G C T T C C A C C G C T T C C A 390
Qy 814 G C C C A C C T A C C T G A C C G C A G A G A T C G A C C T G C C A C C C A C C A C C A T C T C G T G T C A G A 873
Db 391 G C C C A C C A T A C C G T A C C T G A G A C A G A G A T C G A C C T G C C A C C C A C C A C C A T C T C G T G T C A G A 450
Qy 874 C G G G G A G A G C C C C C A C C C T A C A G G G C C C C T G C A C C C T C C A G C T T C G G A C C C C G A G C A 933
Db 451 C G G G A G A G C C C C C A C C C T A C A G G G C C C C T G C A C C C T C A G C T T C G G A C C C C G A G C A 510
Qy 934 G C A G C T G A A C T G A A C C G G A G T C G T G C G C A C C C C A A A C A G A A C C A T C T T C G A C A G 993
Db 511 G C A G C T G A A C T G A A C C G G A G T C G T G C G C A C C C C A A A C A G A A C C A T C T T C G A C A G 570
Qy 994 T G A C C T G A T G A T G C C A G G C T G G G C G C C C C T G C C C C C C A G C A G T A A C T C G G G C A T 1053
Db 571 T G A C C T G A T G A T G C C A G G C T G G G C G C C C C T G C C C C C C A G C A G T A A C T C G G G C A T 630
Qy 1054 C A G C G C A C A G T G T A C G C A G C G G C G G C G C A T G A G G G G C C G C C C A C C T A C A G C G A 1113
Db 631 C A G C G C A C A G T G T A C G C A G C G G C G G C G C A T G A G G G G C C G C C C A C C T A C A G C G A 690
Qy 1114 G G T A C T G G C C A T A C C C G G G T C C T C T T C C A G C A C C A G C A G A G T G G G C C G C C C T C 1173
Db 691 G G T A C T G G C C A T A C C C G G G T C C T C T T C C A G C A C C A G C A G A G T G G G C C G C C C T C 750
Qy 1174 C T T G C T G A G G A C C C G G C T C C A C A C A C A C A C A T G C G C C C C T A G A G A G C C A G C C A T 1233
Db 751 C T T G T G G A G G A C C C G G C T C C A C A C A C A C A C A T G C G C C C C T A G A G A G C C A G C C A T 810
Qy 1234 C T G G A C A A A G A A G A T A A A C A G A A A G G A C A C C C T C T A G G G T C C C C A G G G G G C G C G 1293
Db 811 C T G G A C A A A G A A G A T A A A C A G A A A G G A C A C C C T C T A G G G T C C C C A G G G G G C G C G 870
Qy 1294 G G C T G G G G T G C T A G T G T A A A A G G C A G 1321
Db 871 G G C T G G G G T G C T A G T G T A A A A G G C A G 898

RESULT 2

US-09-769-482-2
; Sequence 2, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/09/769,482
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 2
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-769-482-2

Query Match 57.2%; Score 755.8; DB 4; Length 759;
Best Local Similarity 99.7%; Pred. No. 6.2e-136;
Matches 757; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 518 A T C A C C G A G C T G G A G T T G T T C A G A T C A T C A T C G T G T G T G A T G A T G T G T G 577
Db 1 A T G G C G G A G C T G G A G T T T G T T C A G A T C A T C A T C G T G T G T G A T G A T G T G T G 60

Qy 578 G T G G T G A T C A C G T G C C T G T G A C C A C T A C A G C T G T C T G C A C G G T C C T T C A T C A C G C G G 637
Db 61 G T G G T G A T C A C G T G C C T G T G A C C A C T A C A G C T G T C T G C A C G G T C C T T C A T C A C G C G G 120
Qy 638 C A C A G C C A G G G C G G A G A G A G A G A T G C C T G T C C T C A G A A G G A T G C C T G T G G C C C T C G 697
Db 121 C A C A G C C A G G G C G G A G A G A G A G A T G C C T G T C C T C A G A A G G A T G C C T G T G G C C C T C G 180
Qy 698 G A G A C A C A G T G T C A G G C A A C G G A T C C C A G A G C C C A G A G T C T A C C C C G C C C T C G G C C 757
Db 181 G A G A C A C A G T G T C A G G C A A C G G A T C C C A G A G C C C A G A G T C T A C C C C G C C C T C G G C C 240
Qy 758 A C C A G C C G C T G C C G T G C C C C T T C G C C C A G A G C G G T T C C A C C G C T T C C A G C C C 817
Db 241 A C C A G C C G C T G C C C C T G C C C C T T C G C C C A G A G G A G C G T T C C A C C G C T T C C A G C C C 300
Qy 818 A C C A T A C C G T A C C T G C A G C A C G A G A T C G A C C T G C C A C C C A C C A C C A T C T C G C T G T C A G A C G G 877
Db 301 A C C A T A C C G T A C C T G C A G C A C G A G A T C G A C C T G C C A C C C A C C A C C A T C T C G C T G T C A G A C G G 360
Qy 878 G A G A G C C C C A C C C T A C A G G G C C C C T G C A C C C T C A G C T T C G G A C C C C G A G A G A G 937
Db 361 G A G A G C C C C A C C C T A C A G G G C C C C T G C A C C C T C A G C T T C G G A C C C C G A G A G A G 420
Qy 938 C T G G A A C T G A A C C G G A G T C G G T G C G C A C C C C C A A A C A G A A C C A T C T T C G A C A G T G A C 997
Db 421 C T G G A A C T G A A C C G G A G T C G G T G C G C A C C C C C A A A C A G A A C C A T C T T C G A C A G T G A C 480
Qy 998 C T G A T G A T A G T G C C A G G C T G G G C G C C C C T G C C C C C C A G C A G T A A C T C G G G C A T C A G C 1057
Db 481 C T G A T G A T A G T G C C A G G C T G G G C G C C C C T G C C C C C C A G C A G T A A C T C G G G C A T C A G C 540
Qy 1058 G C C A C G T G T A C G G C A G C G G G C G C A T G A G G G G C C C C C C C A C C T A C A G C A G G T C 1117
Db 541 G C C A C G T G T A C G G C A G C G G G C G C A T G A G G G G C C C C C C C A C C T A C A G C A G G T C 600
Qy 1118 A T C G G C A C T A C C C G G G T C C T C T T C A G C A C C A G C A G C A G T G G G C G C C C T C C T T G 1177
Db 601 A T C G G C A C T A C C C G G G T C C T C T T C A G C A C C A G C A G C A G T G G G C G C C C T C C T T G 1177
Qy 1178 C T G A G G G A C C C G C T C C A C A C A C A C A C A T C G C G C C C T A G A G A G C A G C C A T C T G 1237
Db 661 C T G A G G G A C C C G C T C C A C C A C A C A C A C A C A T C G C G C C C T A G A G A G C A G C C A T C T G 720
Qy 1238 A C C A A G A A G A G A T A A C A G A A A G A C A C C C T C T C T A G 1276
Db 721 A G C A A G A A G A G A T A A A C A G A A A G G A C A C C C T C T C T A G 759

RESULT 3

US-09-091-952A-7
; Sequence 7, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla b.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834

```
;
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLYING APPLICATION NUMBER: US/09/091,952A
;   FILING DATE: 19-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/029,278
;   FILING DATE: 28-OCT-1996
;   APPLICATION NUMBER: PCT/US97/19381
;   FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, Timothy L.
;   REGISTRATION NUMBER: 35,367
;   REFERENCE/DOCKET NUMBER: 015280-297100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 921 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 1...921
;   OTHER INFORMATION: Clone 22 coding region
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
;
US-09-091-952A-7
;
Query Match      26.7%; Score 352.2; DB 3; Length 921;
Best Local Similarity 73.1%; Pred. No. 1.3e-58;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 506 CAGAGCATGAGATCAGCGAGCTGGAGTTGTTTCAGATCATCATCATCGTGGTGGTATG 565
DB 166 CCGGGCATCTTCACTCGGAGCTGGAGTTGCCCAATCATCATCATCGTGGTGGTGC 225
QY 566 ATGGTGATGTTGGTGGTATGATCAGTGCCTGCTGAGGCACATCAAGCTGTCTGCACCGTCC 625
DB 226 ACGGTGATGTTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 285
QY 626 TTATCATGCGCGGACAGCGAGCGGGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGC 695
DB 286 TTATCAACCGCGCGAACCAGAGCGGAGCGGGGAGGAGCGGGTGGCGGAGGAGGATGC 345
QY 686 CTGTGCGCTTCGAGAGCAGATGTCAGGCAACGGAATCCAGAGCGCGAGGCTACGCC 745
DB 346 CTGTGCGCTTCAGAGCGCGCGGACCGCGGCTGG-----CGCTCGGAGATCATGCAT 399
QY 746 CCGCTCGCGCCACCGACCGCTGGCGGTGGCGCGCTTCGCCCGAGCGGAGCGCTTCCAC 805
DB 400 GCGCGCGGTCCAGGAGACAGTTTCAGAGCGCGCTTCCTCATCAGAGGATCGCTTCAGC 459
QY 806 CGCTTCAGCGCCACTATTCGTATCCTGTCAGCAGAGATGACCTGCCACCCACATCTCG 865
DB 460 CGCTTCAGCGCCACTATTCGTATGTCAGCAGAGATGATCTTCTCCACCATCTCC 519
QY 866 CTGTGAGCGGGAGGAGCGCCACCTACAGGGCGCTGCACCTCCAGCTTCGGGAC 925
DB 520 CTGTCCGACGGTGAAGAGCACCTCTCTTACAGGGCGCTTCGACCTTCGAGCTCCGGGAC 579
QY 926 CCGAGCAGCAGCTGGAATGAACCGGGAGTCGGTGGCGCACCGCCCAACAGAACCATC 985
DB 580 CTTGAACAGCAGATGGAACTCAACCGAGATCGGTGAGGCGCCCAACCAACCACTA 639
QY 986 TTCGACAGTACCTGATGGATAGTGCCAGG---CTGGGCGGCGCCCTGTGCCCCCGGAGCAGT 1042

;
;
; Db 640 TTTGACAGTGATTATATAGACATTGTATGTATAGCGGGGTCATGTCACCCAGCAGC 699
; QY 1043 AACTCGGGCATCAGCCCGCTAGCTACGCGAGCGGGGCGGCGATGAGAGGGGCGCGCC 1102
; Db 700 AACTCGGGCATCAGTCAAGCAGCCTGTCAGCAGTAACGGGAGGATGAGAGGGGCGCACCC 759
; QY 1103 ACCTACAGCGAGGTATCGGCCACTACCGGGGTCTCTTCCAGCAGCAGCAGCAGCAG 1161
; Db 760 ACATACAGCGAGGTATGCGGCCACCCAGCGGCGCTCTTCTCATCACCAGCGGAG 818
;
;
; RESULT 4
; US-09-091-952A-6
; Sequence 6, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic
; CORRESPONDENCE ADDRESS: Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/091,952A
;   FILING DATE: 19-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 60/029,278
;   FILING DATE: 28-OCT-1996
;   APPLICATION NUMBER: PCT/US97/19381
;   FILING DATE: 28-OCT-1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Smith, Timothy L.
;   REGISTRATION NUMBER: 35,367
;   REFERENCE/DOCKET NUMBER: 015280-297100US
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 8065 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
;   NAME/KEY: -
;   LOCATION: 1...8065
;   OTHER INFORMATION: Clone 22
; FEATURE:
;   NAME/KEY: CDS
;   LOCATION: 116...1036
;   OTHER INFORMATION: Clone 22 coding region
; FEATURE:
```


CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...867
OTHER INFORMATION: Clone 22 isoform 2 alternatively
spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-091-952A-8

Query Match 21.5%; Score 284.2; DB 3; Length 867;
Best Local Similarity 68.7%; Pred. No. 1.3e-45;
Matches 453; Conservative 0; Mismatches 143; Indels 63; Gaps 2;
QY 506 CAGAGATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGATG 565
DB 166 CCGGGCATCTTCAACTCGGAGCTGGAGTTCCGCCAAATCATCATCATCGTGGTGGTG 225
QY 566 ATGCTGATGGTGGTGTGATCATCGTGCCTGAGCCACTACAGCTGTCTGCAAGTCC 625
DB 226 ACGGTGATGGTGGTGTGATCATCGTGCCTGAGCCACTACAGCTGTCTGCAAGTCC 285
QY 626 TTCTATCAGCCGGCAGACCGAGCGGCGGAGGAGAGATGCCCTGTCTCCTCAGAAGGATGC 685
DB 286 TTCTATCAGCCGGCAGACCGAGCGGCGGAGGAGGAGCGGGCT----- 329
QY 686 CTGTGGCCCTCGGAGAGACAGATGTTCAGGCAACGGGAATCCAGAGCGCGAGGTCTAGCC 745
DB 330 -----GCCGAGATCATGTCAT 345
QY 746 CCGCCTCGGCCACCGACCGCCTGGCGGTGCGCCCTTCCGCCAGCGGGAGCGCCTCCAC 805
DB 346 GCCCGCGGTGCGAGGACAGGTTTCAGACCGCGCTCTTCATCCAGAGGGATCCGCTTCAGC 405
QY 806 CGCTTCAGCCCACTATCGTACCTGTCAGCAGAGATCGACCTGCCACCACCATCTCG 865
DB 406 CGCTTCAGCCCACTATCGTACCTGTCAGCAGAGATGATCTCTCCACCATCTCC 465
QY 866 CTGTACAGCGGGAGGAGGAGCGCCCACTACAGGGCGCCCTGCACCTCCAGCTTCGGGAC 925

DB 466 CTGTCCGAGCGGTGAAGAGCCACCTCTTACAGGGGCCCTGCACTTCCAGTCCGGGAC 525
QY 926 CCGAGCAGCAGCTGGAACCTGAAACCGGGAGTCCGGTGCAGCACCCTCCAAACAGAACCATC 985
DB 526 CCGTGAACAGCAGATGGAACCTCAACCGAGAGTCCGTGAGGGGCCCAACCAACCGAACCAT 585
QY 986 TTGACAGATGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1042
DB 586 TTGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 645
QY 1043 AACTCGGGCATCAGCGCCAGCTGCTACGCGCGGGCGGCGATGGAGGGGGCGCGCGCC 1102
DB 646 AACTCGGGCATCAGCTGCAAGCACCTGCAAGCACTGCAAGCACTGCAAGCACTGCAAGCA 705
QY 1103 AACTCAGCAGGAGTCTATCGGCCACTACCGGGGCTCTCTTCCAGCACCGAGAGCAG 1161
DB 706 ACATACAGCGAGGTGATGGGCCACCCAGCGGGCGCTCTTTCTCCATCACCAGCGCAG 764
RESULT 7
US-09-621-976-2162
; Sequence 2162, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2162
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162
Query Match 6.8%; Score 90.4; DB 4; Length 391;
Best Local Similarity 75.7%; Pred. No. 1.5e-08;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 1019 GCGGGCCCTGCCCCCGGAGCACTGAGGATGAGGAGGAGGAGGAGGAGGAGGAGGAG 1078
DB 26 GCGGGTCCATGCGCCACCGAGCAACTCGGGCATCATCGGCAAGCACTGCAAGCACTG 85
QY 1079 GCGGCATGAGGGGGCGCGCCCACTACAGGAGGTATCGGCACTACCGGCACTACCGGGTCC 1138
DB 86 GGAGAGATGAGGGGGCGCCACCCCAATACAGGAGGTATGGGCCACCAACCGAGCGCC 145
QY 1139 TCCTTCCAGCACCGAGAGCAGTGGGC 1166
DB 146 TCCTTCCATCACCAGCGCAAGCG 173
RESULT 8
US-09-616-289-48/c
; Sequence 48, Application US/09616289
; Patent No. 6632923
; GENERAL INFORMATION:
; APPLICANT: Lees, Ann M.
; APPLICANT: Lees, Robert S.
; APPLICANT: Law, Simon W.
; APPLICANT: Arjona, Anibal A.
; TITLE OF INVENTION: NOVEL LOW DENSITY LIPOPROTEIN BINDING
; TITLE OF INVENTION: PROTEINS AND THEIR USE IN DIAGNOSING AND TREATING
; TITLE OF INVENTION: ATHEROSCLEROSIS
; FILE REFERENCE: 10797-004001

98	QY	GCTAGCGG	CAGAGGCT	CAGCCCCCGGCGG	CAGCGCGGCCCCGCTG	CGAGCCCA	TTTCCG	157
24175	Db	GCAGCCCCCGG	AGAGCCCCCGG	CGAGCCCCCGG	AGCCCCCGG	AGCCCCCGG	AGCCCCCGG	24116
158	QY	GAGCGCA	CCCGCGG	CATCGC	GACGCC	CCCGGGG	CTGCCAGGGAGG	CCGGGGGGCG
								217
24115	Db	GAGCCCCCGG	AGAGCCCCCGG	CAGCCCCCGG	CAGCCCCCGG	CAGCCCCCGG	CAGCCCCCGG	24056
218	QY	CAGCGAG	CGGCTCC	CGCGCA	TGAGCC	CCCGGGG	CCCGGGGAA	CTTGGCGCGCACCC
								277
24055	Db	CCCCCGG	CAGCCCCCGG	AGCCCCCGG	AGCCCCCGG	AGCCCCCGG	AGCCCCCGG	23996
278	QY	GAGCCCGG	AGAGCGGGG	CGCGCT	CTCCCGCGCGG	CGCTCT	CTGATGCGGGG	CCCCAG
								337
23995	Db	CCCCCGG	AGCCCCCGG	CGAGCCCCCGG	AGCCCCCGG	AGCCCCCGG	AGCCCCCGG	23936
338	QY	CTTCGGG	CGCGCGAG	CCCCCGCGG	CGCGCGCCCCCGG	CGAGCCCCCGG	CGCGCGCCCCCGG	CGCGCG
								397
23935	Db	CCGCGAG	CCCCCGG	AGCCCCCGG	AGCCCCCGG	AGCCCCCGG	AGCCCCCGG	23876
398	QY	GCGCGCGG	CGGTC	CATGCA	CCG			420
23875	Db	GCAGCCCCCGG	CGCCCTG	CACTG				23853

```

RESULT 11
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequ
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

```

Query Match	5.3%;	Score 70.4;	DB 3;	Length 4403765;
Best Local Similarity	50.0%;	Pred. No. 0.00046;		
Matches 230;	Conservative 0;	Mismatches 226;	Indels 4;	Gaps 2;
QY	2	GACCGCGGTCTCGAGCGAAACCGATCTCTCTTGGACTTCGAATCAGGAGGAGGAGGCGCG	61	
Db	3936335	GCCGGCGGCAACGGCGGCA	CGGCGGCGAGAGGCGGCGAGTGGTGGCGCCGCGGCGGACGGT	3936394
QY	62	GGCGGCGCGCGCGCGGAGGCGTTCGGCTGGGGAAAGCTAGCGGCAAGAGCTTCAGCCCCG	121	
Db	3936395	ATCGTGGCGTTCGCGCGCGGCAAGGCGGCGCAACGGCGCGGACGCGCAAGTCGGCGGTGCG	3936454	
QY	122	CGGCGAGCGGCGCGCCCGCTGCCAGCCCATTTTCGGACGCGCACCCCGGGGCACTGCCG-	180	
Db	3936455	GGCGGCGCGGCGGACGCGGCGCCAAACACAGTCCCGCGGCGCACGCGCGGCAAGAGGT	3936514	
QY	181	-ACGCCCCCGGGGTTCGCGAGGGGAGGCGCGGGGGGCGCGAGCGGAGCGCGGTCCCGCGCA	239	
Db	3936515	CAAGCGGCGAGCGTGGTCCGCTGGGGCGGCGCGGGGCTGGCGGCGCGGTGGGGGCGCT	3936574	
QY	240	CTGAGCCCCCGGCGCCCGCGGAACCTTGGCGGCGACCCGAGCCCGGCGCGCGGGGCGCG	299	

Db	3936575	AACGGCACCGCTGGCAACGGCGGCCAAGCGGGTGTCCCGGCGCACCGGAGGCGCCGCGCGCA	3936634
Qy	300	CTTCTCCCCCGCGCGCCCTCTCTGATGCGGGGGCCCCAGCTCGGGGCGCGCGCGCGAGCCC	359
Db	3936635	GCCTCTCTAGCTACCAACGGCGGCGACGGCGCGCGCGG--CGGCACCGGAGGCGCAGCGG	3936692
Qy	360	CCCCCGCGCGCCCCCGAGCCCCCGCGCCCCCGCGCGCGCGCGCGCGTTCATGCACC	419
Db	3936693	GCACGCGCGCGCGCGCGGCACCGGAGGCGCGCGCGGCACCGCGGGGCGCGCGCGACG	3936752
Qy	420	GCTTGATGGGGTCAACAGCACCGCCCGCGCGCGCGCGCGG	459
Db	3936753	GCAGCAAGAGTGGCCAGGGCGGGCGCGCGGGGGGGTTCGGG	3936792

RESULT 12

```

US-09-949-016-17015
; Sequence 17015, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 17015
; LENGTH: 13343
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17015

```

Query Match	5.3%;	Score 69.4;	DB 4;	Length 13343;
Best Local Similarity	51.9%;	Pred. No. 0.00028;		
Matches 182; Conservative	0;	Mismatches 166;	Indels 3;	Gaps 1;
Qy	50	GGAGGAGCGCGCGCGCGCGCGCGCGCGCGCTCGGCTGGGGAAAGCTACGGGCAGA	109	
Db	2441	GGGGCCCGCGCGCGCGCGCGCGAGGGGGCGCCCCGCCGCCGACGTTCGCCCTTCC	2500	
Qy	110	GGCTCAGCCCGCGCGGCGAGCGCGCGCCCCTGCTGCC---AGCCCATTTTCGGGACGCCACC	166	
Db	2501	TCCAGCCCGCGGGGTGCGAGCGCGCGCGCTTATTCCAGGCGCGGGCGGCGCG	2560	
Qy	167	CGCGGGCACTGCGCAGCGCCCGCGGGGTGCCGAGGGGAGGCGCGGGGGGGCGCAGCGGAGC	226	
Db	2561	ACCGCGCGCGGGGAGGGCGCGCGCGCGGGGGCGGGCGGGCGCGCGCGCGGG	2620	
Qy	227	GCGGTCCCGGCACTGAGCCCGCGCGCGCCCGGGGAAC TTGGCGGGCACCCGAGCCCGCGC	286	
Db	2621	GAGGACCGCCGACCCCTTTCCCGCGCGCGGGGGCCCCCTGCGGGGGGGCGGGGACCCGGGA	2680	
Qy	287	GAGCCCGGGCGCGCCTCCCCCGCGCGCGCGCTCCTGCATGCGGGGGCCCCCAGCTCCGGGGCG	346	
Db	2681	AAGCGCGCGGTGGGGAGGGGCGCGCAGCTGCGGGGAGCGGAGTTGTGCACCCCGCGCG	2740	
Qy	347	CCGGCCGGAGCCCCCCCCCGCGCGCGCCCCCGAGCCCCCGCGCGCCCCCGCGCGCGC	397	
Db	2741	GAGCCCGGAGGAGCCCGGGCGCACTGCGCGGGCGGGCGGTCTCCGCTCGGAGC	2791	

RESULT 13
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328

GENERAL INFORMATION:
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
FILE REFERENCE: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 4411529
TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 5.2%; Score 68.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 0.00093;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;
Matches 229; Conservative 0; Mismatches 227; Indels 4; Gaps 2;

QY 2 GACCGGGTCTCGAGGGAACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGGC 61
Db 3942788 GCCGGGGCAACCGCGGCACCGCGCGCAGAGCGCGAGTGGTGGCGCGCGCGACGGT 3942847

QY 62 GCGCGCGCGCGCGCGCGCGCTCGGCTGGGGAAGCTAGCGGCGAGAGGCTCAGCCCCG 121
Db 3942848 ATCGTGGGTGCGCGCGCGCGCAAGGCGGCAACGCGCGCGAGCGGCGGCGGTGCG 3942907

QY 122 GCGCGAGCGCGCGCGCGCTGCGCGAGCCCAATTTTCGAGAGCCACCGCGCGGCACTCCCG- 180
Db 3942908 GCGCGCGCGCGCGCGCGCGCCCAACACCGTCCCGCGGCAACCGCGCGGCAAGGT 3942967

QY 181 -ACGCCCCCGGGCTCGAGGAGGAGCGCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCA 239
Db 3942968 CAAGCGCGCGCGCGCGCGCGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 3943027

QY 240 CTGAGCGCGCGCGCGCGCGCGCGGGAACCTTGGCGGCGACCCGAGCGCGCGCGCGCGCG 299
Db 3943028 AACGGACCGCTGGCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCA 3943087

QY 300 CTCTCCCGCGCGCGCGCTCTGATGCGGGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 359
Db 3943088 GCCTCTCAGTACCAACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3943145

QY 360 CCG 419
Db 3943146 GCAGCG 3943205

QY 420 GCTTGATGGGCTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 459
Db 3943206 GCGGACAAGTGGCCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 3943245

RESULT 14
US-09-949-016-13845/c
Sequence 13845, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12371
LENGTH: 152145
TYPE: DNA
ORGANISM: Human
US-09-949-016-12371

Query Match 5.2%; Score 68.4; DB 4; Length 152145;
Best Local Similarity 51.1%; Pred. No. 0.00065;
Matches 186; Conservative 0; Mismatches 176; Indels 2; Gaps 1;
Matches 186; Conservative 0; Mismatches 176; Indels 2; Gaps 1;

QY 109 AGGCTCAGCCCCCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 168
Db 2063 ATGCTGAGGCG 2004

QY 169 CGGGCACTGCGGACG 228
Db 2003 CACACTGAGCTGAGCG 1944

QY 229 GGTCCCGCGCACTGAGCG 288
Db 1943 GTCTGCTGCTGCGGTACCATGCAACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1884

QY 289 GCGCGGCGCGCGCTCCCG 348
Db 1883 GCGCAGCGCGCGCTCCG 1826

QY 349 GCGCGGAGCG 408
Db 1825 GAGGGGGAGCTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1766

QY 409 GTCCATGCAACCGCTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCG 468
Db 1765 GCGAGCG 1706

QY 469 TGTC 472
Db 1705 TGCG 1702

RESULT 15
US-09-949-016-12371/c
Sequence 12371, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949, 016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12371
LENGTH: 152145
TYPE: DNA
ORGANISM: Human
US-09-949-016-12371

Query Match 5.2%; Score 68.4; DB 4; Length 152145;
Best Local Similarity 51.1%; Pred. No. 0.00065;
Matches 186; Conservative 0; Mismatches 176; Indels 2; Gaps 1;
Matches 186; Conservative 0; Mismatches 176; Indels 2; Gaps 1;

QY 109 AGGCTCAGCCCCCGGCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 168
Db 2063 ATGCTGAGGCG 2004

```
Qy 169 CGGCACTGCGAGCCCGCGGCTGCCGAGGGGCGCGGGGGCGCAGCGAGCGC 228
Db 2003 CACACTGAGCTGAGCCCGACCGGACCGGGCTGGCGCTGGGGCCGCTGCTGTGGCG 1944
Qy 229 GGTCCCGCGCACTGAGCCCGCGCGCCCGGGAACTTGGCGGCGACCCGAGCCCGCGCGA 288
Db 1943 GCTGCTGCTGCGGTTACCATGGCAACCCCGGGCCCGCGCGCGCGCGCGCGCGCGA 1884
Qy 289 GCCGGGGCGGCGCTTCCCGCGCGCGCGCTTCTGCAATGCGGGGCCCGCAGCTCCGGGGCGC 348
Db 1883 GCCCAGCGCCCGCTCCGC--CCGCGAGGGGGCGGCTTCCGCGCGCGGGGCCCGGGCCG 1826
Qy 349 GCGCGGAGCCCCCGCGCGCCCGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGC 408
Db 1825 GGAGGGGGACGTGGCGGGGGCGGGCCGAGCTCCCGCGCTTGGCGCTCTTTCCCGCG 1766
Qy 409 GTCCATGCAACCGCTTGATGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCA 468
Db 1765 GGGAGCGCGGCGCGGGGGCGCTGGGAGCCGCGAGGGGGCGTCTGCGCGCGCGCTGTCCCT 1706
Qy 469 TGTC 472
Db 1705 TGGC 1702
```

Search completed: February 19, 2005, 16:22:50
Job time : 260.374 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 14:21:20 ; Search time 742.23 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgcacgcgtctcgagcgca.....ctgcgtagtgaaagcgag 1321

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs, 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq.*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq.*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq.*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq.*
- 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq.*
- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq.*
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1321	100.0	1321	9 US-09-934-249-1	Sequence 1, Appli
2	1229	93.0	4839	15 US-10-241-220-119	Sequence 119, App
3	1229	93.0	4839	16 US-10-269-909-84	Sequence 84, Appl
4	1229	93.0	4839	16 US-10-269-909-85	Sequence 85, Appl
5	1229	93.0	4839	18 US-10-872-972-119	Sequence 119, App
6	1229	93.0	4839	18 US-10-872-991-119	Sequence 119, App
7	864	65.4	864	17 US-10-295-027-127	Sequence 127, App
8	861	65.2	861	9 US-09-934-249-3	Sequence 3, Appli
9	803.2	60.8	969	10 US-09-796-753-55	Sequence 55, Appl
10	802.2	60.7	1141	15 US-10-205-823-412	Sequence 412, App
11	802.2	60.7	1141	15 US-10-301-822-208	Sequence 208, App

12	802.2	60.7	1850	15	US-10-241-220-44	Sequence 44, Appl
13	802.2	60.7	1850	18	US-10-872-972-44	Sequence 44, Appl
14	802.2	60.7	1850	18	US-10-872-991-44	Sequence 44, Appl
15	802.2	60.7	4527	10	US-09-821-813-2	Sequence 2, Appli
16	802.2	60.7	4527	18	US-10-849-635-2	Sequence 2, Appli
17	801.6	60.7	1140	16	US-10-390-045-1	Sequence 1, Appli
18	801.6	60.7	1140	17	US-10-434-479-1	Sequence 1, Appli
19	790.4	59.8	1086	13	US-10-098-841-71	Sequence 71, Appl
20	767.4	58.1	806	15	US-10-241-220-45	Sequence 45, Appl
21	767.4	58.1	806	18	US-10-872-972-45	Sequence 45, Appl
22	767.4	58.1	806	18	US-10-872-991-45	Sequence 45, Appl
23	755.8	57.2	759	16	US-10-390-045-2	Sequence 2, Appli
24	755.8	57.2	759	17	US-10-434-479-2	Sequence 2, Appli
25	616.4	46.7	878	9	US-09-934-249-12	Sequence 12, Appl
26	589.2	44.6	1583	14	US-10-000-256A-32	Sequence 32, Appl
27	493.6	37.4	693	9	US-09-934-249-14	Sequence 14, Appl
28	466.2	35.3	1713	10	US-09-796-753-57	Sequence 57, Appl
29	352.2	26.7	921	16	US-10-251-598-7	Sequence 0, Appli
30	352.2	26.7	8018	13	US-10-087-192-1667	Sequence 1667, Ap
31	352.2	26.7	8065	16	US-10-251-598-6	Sequence 0, Appli
32	350	26.5	920	9	US-09-823-245A-20	Sequence 20, Appl
33	350	26.5	2170	17	US-10-094-749-197	Sequence 197, App
34	349	26.4	8093	9	US-09-934-249-16	Sequence 16, Appl
35	349	26.4	8093	17	US-10-172-118-1023	Sequence 1023, Ap
36	349	26.4	8093	17	US-10-342-887-1023	Sequence 1023, Ap
37	341.8	25.9	475	9	US-09-934-249-15	Sequence 15, Appl
38	298	22.6	837	18	US-10-363-345A-30089	Sequence 30089, A
39	298	22.6	837	18	US-10-363-345A-30090	Sequence 30090, A
40	284.2	21.5	867	16	US-10-251-598-8	Sequence 0, Appli
41	270.8	20.5	837	18	US-10-363-345A-30091	Sequence 30091, A
42	270.8	20.5	837	18	US-10-363-345A-30092	Sequence 30092, A
43	250.2	18.9	285020	13	US-10-087-192-1666	Sequence 1666, Ap
44	182	13.8	368	9	US-09-783-590-3464	Sequence 3464, Ap
45	182	13.8	467	10	US-09-918-995-2074	Sequence 2074, Ap

ALIGNMENTS

RESULT 1

US-09-934-249-1
; Sequence 1, Application US/09934249
; Patent No. US20020115081A1
; GENERAL INFORMATION:
; APPLICANT: Lee, Richard T.
; APPLICANT: Landschulz, Katherine T.
; APPLICANT: Turi, Thomas G.
; APPLICANT: Thompson, John F.
; APPLICANT: Kennedy, Scott P.
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
; FILE REFERENCE: P0738/7001/ERP/KA
; CURRENT APPLICATION NUMBER: US/09/934, 249
; CURRENT FILING DATE: 2001-08-21
; PRIOR APPLICATION NUMBER: US 60/227,159
; PRIOR FILING DATE: 2000-08-22
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 1321
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (413)...(1273)
US-09-934-249-1

Query Match 100.0%; Score 1321; DB 9; Length 1321;
Best Local Similarity 100.0%; Pred. No. 2.8e-310;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGACCGCGTCTCGAGCGCAACCCGATCTCTTGACTTGATGAGGAGGAGCGG 60
|||||

Db	1	CGACCGCGGTCTCGAGACGAAACCCGATCTCTCTTGGACTTGAATGAGGAGGAGAGGCGG	60
Qy	61	CGGCGGCGGCGCGCGAGAGCGCTCGGCTGGGAAAGTAGCGGCAGAGGCTCAGCCCC	120
Db	61	CGGCGGCGGCGCGGAGGCGCTCGCTGGGAAAGCTAGCGGACAGGCTCAGCCCC	120
Qy	121	GGGCGAGCGGCGCCCGCTGCGAGCCCATTTTTCGGACGCCACCCGCGGGGCACTGC	180
Db	121	GGGCGAGCGCGCGCCCGCTGCGAGCCCATTTTTCGGACGCCACCCGCGGGGCACTGC	180
Qy	181	ACGCCCCGGGGCTGCGAGGGGAGGCGGGGGGGCGCAGCGGAGCGCGTCCGCGCAC	240
Db	181	ACGCCCCGGGGCTGCGAGGGGAGGCGGGGGGGCGCAGCGAGCGCGTCCGCGCAC	240
Qy	241	TGAGCCCCGGCGCCCGCGGAACTTTCGGCGGACCCGAGCCGCGGAGCGCGGGCGCGC	300
Db	241	TGAGCCCCGGCGCCCGCGGAACTTTCGGCGGACCCGAGCCGCGGAGCGCGGGGCGCGC	300
Qy	301	CTCCCCCGCGCGCTCTCTGCATGCGGGCCCCAGCTCCGGGCGCGCGCGAGCGCCCC	360
Db	301	CTCCCCCGCGCGCTCTCTGCATGCGGGCCCCAGCTCCGGGCGCGCGCGAGCGCCCC	360
Qy	361	CCCCGGCGCCCGGAGCCCCCGCGCCCGCGGCGCGCGCGCGCGCGCTCATGCACCG	420
Db	361	CCCCGGCGCCCGGAGCCCCCGCGCCCGCGGCGCGCGCGCGCGCGCTCATGCACCG	420
Qy	421	CTTGATGGGGTCAACAGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGTCA	480
Db	421	CTTGATGGGGTCAACAGCACCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCTTGTCA	480
Qy	481	GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTGTTC	540
Db	481	GTGCAACTGCAAACGCTCTTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTGTTC	540
Qy	541	GATCATCATCATCGTGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	600
Db	541	GATCATCATCATCGTGTGTGATGATGTGTGTGTGTGTGTGTGTGTGTGTGTGTG	600
Qy	601	CCACTAAGCTGTCTCAGCGTCTTTTCATCAGCCGCGCACAGCCGCGGCGGAGAGAG	660
Db	601	CCACTAAGCTGTCTCAGCGTCTTTTCATCAGCCGCGCACAGCCGCGGCGGAGAGAG	660
Qy	661	AGATGCCCTGTCTCAGAAGGATGCTGTGGCCCTCGGAGAGCACAGTGTCAAGCAACGG	720
Db	661	AGATGCCCTGTCTCAGAAGGATGCTGTGGCCCTCGGAGAGCACAGTGTCAAGCAACGG	720
Qy	721	AATCCGAGAGCGGAGTCTTAGCCCCGCTCGGCCCAACCGACGCTGCGCTGCGCGCC	780
Db	721	AATCCGAGAGCGGAGTCTTAGCCCCGCTCGGCCCAACCGACGCTGCGCTGCGCGCC	780
Qy	781	CTTCGCCACGGGAGCGCTTCCACCGCTTTCAGCCACCTATCCGTACCTGCGAGCACA	840
Db	781	CTTCGCCACGGGAGCGCTTTCAGCCGTTTCAGCCACCTATTCGGTACCTGCGAGCACA	840
Qy	841	GATCGACTGCAACCCATCTCGCTGTGAGACGGGGAGGAGCCCCACCTTACAGGG	900
Db	841	GATCGACTGCCACCCATCTCGCTGTGAGACGGGGAGGAGCCCCACCTTACAGGG	900
Qy	901	CCCTGTGACCTTCAGCTTCGGGACCCGAGAGCAGCTGGAACCTGAAACGGGAGTGGT	960
Db	901	CCCTGTGACCTTCAGCTTCGGGACCCGAGAGCAGCTGGAACCTGAAACGGGAGTGGT	960
Qy	961	GGCGCACCCCCAAGACCATCTTTCGACAGTGACCTGATGGATGTGCCAGGCTGG	1020
Db	961	GGCGCACCCCCAAGACCATCTTTCGACAGTGACCTGATGGATGTGCCAGGCTGG	1020
Qy	1021	CGGCCCCCTGCCCCCCCAGCAGTAACCTCGGCGATCAGCGCACCTGTGTACGGCAGCGCGG	1080
Db	1021	CGGCCCCCTGCCCCCCCAGCAGTAACCTCGGCGATCAGCGCACCTGTGTACGGCAGCGCGG	1080
Qy	1081	CGCGATGAGAGGGCGCGGCCACCTTACAGCGAGGTCATCGGCCATCTACCCGGGGTCTC	1140
Db	1081	CGCGATGAGAGGGCGCGGCCACCTTACAGCGAGGTCATCGGCCATCTACCCGGGGTCTC	1140

RESULT 2

```

US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-241-220-119

```

Query Match	93.0%;	Score 1229;	DB 15;	Length 4839;
Best Local Similarity	100.0%;	Pred. No. 5.7e-288;		
Matches 1229;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	93	GGAAAGCTAGCGCAGAGGCTCAGCCCGCGCGGCGACGCGCGCGCCCGCTGCTGCCAGCCCA	152
Db	1	GGAAAGCTAGCGCGAGAGGCTCAGCCCGCGCGCGCGCGCGCGCTGCCAGCCCA	60
Qy	153	TTCCGAGACGCCACCCCGGGGCACTGCGCAGCGCCCCCGGGGCTGCGAGGGGAGCGCGGG	212
Db	61	TTCCGAGACGCCACCCCGGGGCACTGCGCAGCGCCCCCGGGGCTGCGAGGGGAGCGCGGG	120
Qy	213	GGCGCGCAGCGGAGCGGCTCCCGCGCACTGAGCGCCCGCGCGCGCCCGGGNACTTGGCGGC	272
Db	121	GGCGCGCAGCGGAGCGGCTCCCGCGCACTGAGCGCCCGCGCGCGCCCGGGAACTTGGCGGC	180
Qy	273	GACCCGAGCCCGCGAGCGGGGCGGCGCTCCCGCGCGCGGCGCTCTGTCATGCGGGGC	332
Db	181	GACCCGAGCCCGCGAGCGGGGCGGCGCTCCCGCGCGCGGCGCTCTGTCATGCGGGGC	240
Qy	333	CCGAGCTCCGGGCGCGGGCGCGAGCGCCCCCGCGCGCGCCCCCGAGCGCCCCCGCGCCCCGC	392
Db	241	CCGAGCTCCGGGCGCGGGCGCGAGCGCCCCCGCGCGCGCCCCCGAGCGCCCCCGCGCCCCGC	300
Qy	393	GC CGCGCGCGCGCGCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCG	452
Db	301	GC CGCGCGCGCGCGCGTCCATGCACCGCTTGATGGGGGTCAACAGCACCGCGCGCGCGCG	360
Qy	453	CCGCGCGGCGAGCCCAATGCTCCTGCA CGTGCAACTGCAGAAACGCTCTTTGTTCCAGAGCA	512


```

; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412

```

Query Match	60.7%	Score 802.2	DB 15	Length 1141
Best Local Similarity	98.4%	Pred. No. 1.3e-184		
Matches 810	Conservative 0	Mismatches 13	Indels 0	Gaps 0
Qy	499	TTTGTTCAGAGCATGGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT	558	
Db	77	TCTCTTCGAAACAGGCAATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGT	136	
Qy	559	GGTGATGATGATGATGTTGGTGGTGATCAGTGTCTCTGTGAGCCACTTACAAGCTGTCTCG	618	
Db	137	GGTGATGATGATGATGTTGGTGGTGATCAGTGTCTCTGTGAGCCACTTACAAGCTGTCTCG	196	
Qy	619	ACGTCTCTTCATCAGCCGCGCACGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGA	678	
Db	197	ACGTCTCTTCATCAGCCGCGCACGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGA	256	
Qy	679	AGGATGCTGTGGCCCTCGGAGAGCAAGTGTTCAGGCAACGGAAATCCAGAGCGCGAGGT	738	
Db	257	AGGATGCTGTGGCCCTCGGAGAGCAAGTGTTCAGGCAACGGAAATCCAGAGCGCGAGGT	316	
Qy	739	CTACGCCCGCGCTCGGCCACCGACCGCTGGCCGTGCCGCCCTTTCGCCCAGCGGGAGCG	798	
Db	317	CTACGCCCGCGCTCGGCCACCGACCGCTGGCCGTGCCGCCCTTTCGCCCAGCGGGAGCG	376	
Qy	799	CTTCCACCGCTTCAGCGCCACTATCCGTACTCTGCAGCAGAGATGCACCTGCCACCCAC	858	
Db	377	CTTCCACCGCTTCAGCGCCACTATCCGTACTCTGCAGCAGAGATGCACCTGCCACCCAC	436	
Qy	859	CATCTCGTGTTCAGACGGGAGGAGCCCCACCTTACAGAGGCCCTTCGACCTTCCAGCT	918	
Db	437	CATCTCGTGTTCAGACGGGAGGAGCCCCACCTTACAGAGGCCCTTCGACCTTCCAGCT	496	
Qy	919	TCGGGACCCCGAGCAGCAGCTGGAACTGAACCCGGAGTTCGGTGCAGCACCACAAACAG	978	
Db	497	TCGGGACCCCGAGCAGCAGCTGGAACTGAACCCGGAGTTCGGTGCAGCACCACAAACAG	556	
Qy	979	AACCATTTTCGACAGTCACTGATGGATAGTGCACAGCTGGGGGGCCCCCTGCCCCCCCAG	1038	
Db	557	AACCATTTTCGACAGTCACTGATGGATAGTGCACAGCTGGGGGGCCCCCTGCCCCCCCAG	616	
Qy	1039	CAGTAACTTCGGGCAATCAGGCCACGTGCTACGGCAGCGGGGGCGCATGAGAGGGCGCCG	1098	
Db	617	CAGTAACTTCGGGCAATCAGGCCACGTGCTACGGCAGCGGGGGCGCATGAGAGGGCGCCG	676	
Qy	1099	GCCCACTTACAGCGAGGTTCATCGGCCCACTACCCGGGGTCTCTCTTCCAGCACACAGAG	1158	
Db	677	GCCCACTTACAGCGAGGTTCATCGGCCCACTACCCGGGGTCTCTCTTCCAGCACACAGAG	736	
Qy	1159	CAGTGGGCGGCCCTCTCTTGTGGAGGGGACCCGGCTCCACACACACATCGCGCCCT	1218	

Db	737	CAGTGGCGCCCTCTCTTGTCTGGAGGGACCGGCTCCACCACACACATCGCGCCCT	796
Qy	1219	AGAGAGCGGACCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGG	1278
Db	797	AGAGAGCGGACCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCTCTCTAGG	856
Qy	1279	TCGCCAGGGGGCGGGCTCGTAGGTGAAAGGCAG	1321
Db	857	TCGCCAGGGGGCGGGCTCGTAGGTGAAAGGCAG	899

RESULT 11
US-10-301-822-208
; Sequence 208, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Thibodeau, Stephen N.
; APPLICANT: Burgart, Lawrence J.
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF COLON CANCER
; FILE REFERENCE: MEM01-029P2RNM
; CURRENT APPLICATION NUMBER: US/10/301,822
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 60/339,971
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/361,978
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/381,988
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 228
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 208
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo Sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96) ... (854)
US-10-301-822-208

Query Match	60.7%	Score	802.2;	DB	15;	Length	1141;		
Best Local Similarity	98.4%;	Pred. No.	1.3e-184;						
Matches	810;	Conservative	0;	Mismatches	13;	Indels	0;	Gaps	0;

Qy	499	TTTGTTCCAGAGATCGGAGATCACGGAGCTGGAGTTGTTCAGATCATCATCATCGTGGT	558
Db	77	TCCTCTCGCAACCGAGCAATGGCGAGCTGGAGTTGTTCAGATCATCATCATCGTGGT	136
Qy	559	GGTGATGATGGTGATGGTGGTGATCACGTCGCCCTGTGAGCCATACAAAGCTGTCTGC	618
Db	137	GGTGATGATGGTGATGGTGGTGATCACGTCGCCCTGTGAGCCATACAAAGCTGTCTGC	196
Qy	619	ACGCTCTTCATCAGCCGGCAGACGACGAGGGCGGAGAGAGATGCCCTGTCTCAGA	678
Db	197	ACGCTCTTCATCAGCCGGCAGACGACGAGGGCGGAGAGAGATGCCCTGTCTCAGA	256
Qy	679	AGGATGCTGTGCCCTTCGGAGAGCACAGTGTCAAGCAGCGAATCCAGAGCCGAGGT	738
Db	257	AGATGCTGTGGCCTTCGGAGAGCACAGTGTCAAGCAGCGAATCCAGAGCCGAGGT	316
Qy	739	CTACGCCCCGCCCTCGGCCACCGAGCCCTGGCCGTGCCGCCCTTCGCCAGCGGAGCG	798
Db	317	CTACGCCCCGCCCTCGGCCACCGAGCCCTGGCCGTGCCGCCCTTCGCCAGCGGAGCG	376
Qy	799	CTTCCACCGCTTCAGCCCAACCTATTCGTTACCTTGACAGCAGAGATCGACTGCCACCCAC	858

Db 377 CTTCCAGCGCTTCCAGGCCCACTATTCGTACTTCGACGACGAGATCGACTGCCACCCAC 436
Qy 859 CATCTCGCTGTACAGCGGGAGAGCCGCCACCTTACAGGGGCCCTGCACCTTCCAGCT 918
Db 437 CATCTCGCTGTACAGCGGGAGAGCCGCCACCTTACAGGGGCCCTGCACCTTCCAGCT 496
Qy 919 TCGGGAACCCGAGCAGCAGCTGGAACTGAAACCGGGAGTCGGTGCAGCACCACCAACAG 978
Db 497 TCGGGAACCCGAGCAGCAGCTGGAACTGAAACCGGGAGTCGGTGCAGCACCACCAACAG 556
Qy 979 AACCATCTTCGACAGTACCTGTGATAGTCAGCAGCTGGGGGCCCTTGCACCCCCACAG 1038
Db 557 AACCATCTTCGACAGTACCTGTGATAGTCAGCAGCTGGGGGCCCTTGCACCCCCACAG 616
Qy 1039 CAGTAACTTCGGGCATCAGCGCCAGCTGCTACGGCAGCGGGCGGCATGAGGGGCCGCC 1098
Db 617 CAGTAACTTCGGGCATCAGCGCCAGCTGCTACGGCAGCGGGCGGCATGAGGGGCCGCC 676
Qy 1099 GCCACCTACAGCAGGTCTATCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGAG 1158
Db 677 GCCACCTACAGCAGGTCTATCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGAG 736
Qy 1159 CAGTGGCGCCCTCTCTTGTGAGGGGACCCGGCTCCACACACACATCGGGCCCT 1218
Db 737 CAGTGGCGCCCTCTCTTGTGAGGGGACCCGGCTCCACACACACATCGGGCCCT 796
Qy 1219 AGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATAAACAGAAAGGACACCCCTCTTAGGG 1278
Db 797 AGAGAGCGCAGCCATCTGGAGCAAGAGAGAGATAAACAGAAAGGACACCCCTCTTAGGG 856
Qy 1279 TCCCGAGGGGGCGGGCTGGGGTGTGCTAGTGTGAAAGGCAG 1321
Db 857 TCCCGAGGGGGCGGGCTGGGGTGTGCTAGTGTGAAAGGCAG 899

RESULT 12

US-10-241-220-44
; Sequence 44, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P50101-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-44

Query Match 60.7%; Score 802.2; DB 15; Length 1850;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;
Qy 499 TTGTGTTCCAGAGCATGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTGCTGCT 558
Db 77 TCTCTCGGNAACAGGCAATGCGAGCTGGAGTTGTTTCAGATCATCATCTGCTGCT 136
Qy 559 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 618
Db 137 GGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 196
Qy 619 ACGGTCTTCATCAGCGGGCAGACCGAGGGGGAGAGAGATGCTCTTCCTCAGA 678

Db 197 ACGGTCTTCATCAGCGGCACAGCCAGCGGCGAGAGAGAGATGCTCTTCCTCAGA 256
Qy 679 AGGATGCTGTGTCGCTTCGAGAGAGCAGTGTGAGCAACGGAATCCGAGCGCGAGGT 738
Db 257 AGGATGCTGTGTCGCTTCGAGAGAGCAGTGTGAGCAACGGAATCCGAGCGCGAGGT 316
Qy 739 CTAGCGCCCGCTTCGCGCCACACCGCTTGGCGCTGCGCCCTTCGCCAGCGGGAGCG 798
Db 317 CTAGCGCCCGCTTCGCGCCACACCGCTTGGCGCTGCGCCCTTCGCCAGCGGGAGCG 376
Qy 799 CTTTCCACCGCTTCAGCCCACTATCTGACCTGACGACGAGATCGACTGTCACCCAC 858
Db 377 CTTTCCACCGCTTCAGCCCACTATCTGACCTGACGACGAGATCGACTGTCACCCAC 436
Qy 859 CATCTCGCTGTACAGCGGGAGAGCCGCCACCTTACAGGGGCCCTTGCACCTTCAGCT 918
Db 437 CATCTCGCTGTACAGCGGGAGAGCCGCCACCTTACAGGGGCCCTTGCACCTTCAGCT 496
Qy 919 TCGGGAACCCGAGCAGCAGCTGGAACTGAAACCGGGAGTCGGTGCAGCACCACCAACAG 978
Db 497 TCGGGAACCCGAGCAGCAGCTGGAACTGAAACCGGGAGTCGGTGCAGCACCACCAACAG 556
Qy 979 AACCATCTTCGACAGTACCTGATGATAGTGTCCAGGCTGGGGCGGCCCTTGCACCC 1038
Db 557 AACCATCTTCGACAGTACCTGATGATAGTGTCCAGGCTGGGGCGGCCCTTGCACCC 616
Qy 1039 CAGTAACTTCGGGCATCAGCGCCAGCTGCTACGGCAGCGGGCGGCATGAGGGGCCGCC 1098
Db 617 CAGTAACTTCGGGCATCAGCGCCAGCTGCTACGGCAGCGGGCGGCATGAGGGGCCGCC 676
Qy 1099 GCCACCTACAGCAGGTCTATCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGAG 1158
Db 677 GCCACCTACAGCAGGTCTATCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGAG 736
Qy 1159 CAGTGGCGCCCTCTCTTGTGAGGGGACCCGGGTTCACACACACATCGGGCCCT 1218
Db 737 CAGTGGCGCCCTCTCTTGTGAGGGGACCCGGGTTCACACACACATCGGGCCCT 796
Qy 1219 AGAGAGCGCAGCCATCTGGAGCAAGAGAGATAAACAGAAAGGACACCCCTCTTAGGG 1278
Db 797 AGAGAGCGCAGCCATCTGGAGCAAGAGAGATAAACAGAAAGGACACCCCTCTTAGGG 856
Qy 1279 TCCCGAGGGGGCGGGCTGGGGTGTGCTAGTGTGAAAGGCAG 1321
Db 857 TCCCGAGGGGGCGGGCTGGGGTGTGCTAGTGTGAAAGGCAG 899

RESULT 13

US-10-872-972-44
; Sequence 44, Application US/10872972
; Publication No. US20040229277A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P50101-US
; CURRENT APPLICATION NUMBER: US/10/872,972
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien

QY 1279 TCCCGAGGGGGCGGGCTGGGGCTGCTAGGTGAAAGGCGAG 1321
Db 857 TCCCGAGGGGGCGGGCTGGGGCTGCTAGGTGAAAGGCGAG 899

RESULT 15

US-09-821-812-2
; Sequence 2, Application US/09821812
; Publication No. US20030166520A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Biaovang
; TITLE OF INVENTION: Androgen Regulated Prostate Specific
; TITLE OF INVENTION: Nucleic Acids
; FILE REFERENCE: P-US 4373
; CURRENT APPLICATION NUMBER: US/09/821,812
; CURRENT FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 4527
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (96)...(851)
US-09-821-812-2

Query Match 60.7%; Score 802.2; DB 10; Length 4527;
Best Local Similarity 98.4%; Pred. No. 1.3e-184;
Matches 810; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 499 TTTGTTCCAGAGCATGAGATACGAGAGTGGAGTTTGTTCAGATCATCATCGTGGT 558
Db 77 TCTCCTCGAAACAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136

QY 559 GGTGATGATGTTGATGTTGTTGATCAGTGCTCTGAGCCACTAGAGCTGTCTGC 618
Db 137 GGTGATGATGTTGATGTTGTTGATCAGTGCTCTGAGCCACTAGAGCTGTCTGC 196

QY 619 ACGTCTCTTCATCAGCGCGCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGA 678
Db 197 ACGTCTCTTCATCAGCGCGCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGA 256

QY 679 AGATGCTGTGGCCCTCGAGAGACACAGTGTGAGCAACGGAATCCAGAGCCGAGGT 738
Db 257 AGATGCTGTGGCCCTCGAGAGACACAGTGTGAGCAACGGAATCCAGAGCCGAGGT 316

QY 739 CTAGCGCCCGCTCGGCCACCGACCGCTGGCGCTGCGCCCTCGCCAGCGGAGCG 798
Db 317 CTAGCGCCCGCTCGGCCACCGACCGCTGGCGCTGCGCCCTCGCCAGCGGAGCG 376

QY 799 CTTCCACCGCTTCAGCGCCACCTATCCGTACCTGCAGCAGATCGACTGCCACCCAC 858
Db 377 CTTCCACCGCTTCAGCGCCACCTATCCGTACCTGCAGCAGATCGACTGCCACCCAC 436

QY 859 CATCTCGCTGTAGAGCGGAGAGAGCCCCACCTACAGGGCCCTGACACCTCCAGCT 918
Db 437 CATCTCGCTGTAGAGCGGAGAGAGCCCCACCTACAGGGCCCTGACACCTCCAGCT 496

QY 919 TCGGGACCCCGAGCAGCAGCTGGAACCTGAACCGGGAGTGGTGCGCGCACCCCAACAG 978
Db 497 TCGGGACCCCGAGCAGCAGCTGGAACCTGAACCGGGAGTGGTGCGCGCACCCCAACAG 556

QY 979 AACCATCTTCAGACAGTGAACCTGATGATAGTGCAGGCTGGGCGGCCCTGCCCCCCCCAG 1038
Db 557 AACCATCTTCAGACAGTGAACCTGATGATAGTGCAGGCTGGGCGGCCCTGCCCCCCCCAG 616

QY 1039 CAGTAATCGGGCATCAGCGCCACGTGCTACGCGCAGCGCGGCGCATGAGAGGGCGGCC 1098
Db 617 CAGTAATCGGGCATCAGCGCCACGTGCTACGCGCAGCGCGGCGCATGAGAGGGCGGCC 676

QY 1099 GCCCACCCTAGCGAGGTCAATCGGCCACTACCGGGGCTCCTCTCCAGCACCAGCAGAG 1158
Db 1158 GCCCACCCTAGCGAGGTCAATCGGCCACTACCGGGGCTCCTCTCCAGCACCAGCAGAG 1158

Db 677 GCCCACCCTAGCGAGGTCAATCGGCCACTACCGGGGCTCCTCTCCAGCACCAGCAGAG 736
QY 1159 CAGTGGGCCGCCCTCCTTGTGCTGGAGGGGACCCGGCTCCACACACACATCGGCCCT 1218
Db 737 CAGTGGGCCGCCCTCCTTGTGCTGGAGGGGACCCGGCTCCACACACATCGGCCCT 796
QY 1219 AGAGAGCGCAGCCCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTCTAGGG 1278
Db 797 AGAGAGCGCAGCCCATCTGGAGCAAGAGAGGATAAACAGAAAGGACACCCCTCTCTAGGG 856
QY 1279 TCCCGAGGGGGCGGGCTGGGGCTGCGTGGTGAAGGAGCAG 1321
Db 857 TCCCGAGGGGGCGGGCTGGGGCTGCGTGGTGAAGGAGCAG 899

Search completed: February 19, 2005, 19:07:12
Job time : 747.23 Secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 10:31:50 ; Search time 4154.31 Seconds
(without alignments)
12103.794 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcggagcga.....ctgcgtagtgaaagggcag 1321

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_hic:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	859.4	65.1	1005	1	AL578575
C 2	858.8	65.0	1038	1	AL517150
C 3	766.8	58.0	967	5	BQ641849
C 4	766	58.0	1046	5	BM922276
C 5	764.2	57.9	1059	1	AL543170
C 6	741	56.1	901	3	CR612083
C 7	736.4	55.7	916	5	BQ954555
C 8	734.2	55.6	850	1	AL558881
C 9	715	54.1	867	5	BX362396
C 10	714.6	54.1	897	1	AL558882
C 11	691.2	52.3	945	5	BUS39219
C 12	686.6	52.0	850	5	BUS39219
C 13	651	49.3	780	9	AY419334
C 14	630.6	47.7	1207	3	AK008976
C 15	618.6	46.8	1079	3	BC023092
C 16	614.6	46.5	782	5	BQ015170
C 17	607.4	46.0	609	5	BQ636742
C 18	588.8	44.6	605	7	QO28567
C 19	578.4	43.8	890	5	BQ690750
C 20	570.4	43.2	973	5	BU169156
C 21	568.8	43.1	572	5	BX641317
C 22	567.4	43.0	729	5	BQ575741
C 23	564.8	42.8	730	4	BM677602
C 24	563.2	42.6	728	5	BU683523

25	550	41.6	551	4	BM141979	BM141979 if25all.y
26	529.8	40.1	894	4	BI851941	BI851941 AGENCOURT
27	521	39.4	1068	5	BUS27705	BUS27705 AGENCOURT
28	507	38.4	780	9	AY419335	AY419335 Pan tregl
29	501.6	38.0	588	4	BM483503	BM483503 536869 MA
C 30	493.6	37.4	693	1	AI761441	AI761441 w65f07.x
C 31	493.4	37.4	655	5	BQ691705	BQ691705 AGENCOURT
32	487.6	36.9	646	9	CG784226	CG784226 FHCC-CGT-
33	486	36.8	1400	4	BM559329	BM559329 AGENCOURT
34	480.8	36.4	964	5	BUS59860	BUS59860 AGENCOURT
35	477.6	36.2	646	5	BUS59841	BUS59841 AGENCOURT
36	476.4	36.1	651	6	CB554226	CB554226 MMSPO052
37	475.2	36.0	624	9	AY419336	AY419336 Mus muscu
38	468.8	35.4	1280	5	BQ691500	BQ691500 AGENCOURT
39	468	35.4	857	4	EG323347	EG323347 602421734
C 40	465.8	35.3	974	2	BB624904	BB624904 BB624904
C 41	465.8	35.3	744	5	BU414421	BU414421 603670223
C 42	461	34.9	763	4	BI646175	BI646175 603276395
C 43	455.4	34.5	629	5	BU730650	BU730650 UI-E-CI1-
C 44	452.2	34.2	618	6	CD367193	CD367193 UI-H-FI2-
C 45	448	33.9	626	5	BM974296	BM974296 UI-CP-EC1

ALIGNMENTS

RESULT 1
LOCUS AL578575/c 1005 bp mRNA linear EST 07-APR-2004
DEFINITION AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
ACCESSION AL578575
VERSION AL578575.3 GI:46257448
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1005)
AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On Feb 16, 2001 this sequence version replaced gi:31316780.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?b=CS0DK001BB12NP1&c=9945.r.

FEATURES

source
1..1005
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK001YC24"
/cell_type="HELA"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 65.1%; Score 859.4; DB 1; Length 1005;
Best Local Similarity 97.7%; Pred. No. 7.1e-150;
Matches 882; Conservative 9; Mismatches 10; Indels 2; Gaps 2;

Qy	878	GAGAGAGCCCCACCTTACCAGGGGCCCTTGACCTTCAGCTTCGGGACCCCGACAGCAG	937
Db	560	GAGAGAGCCCCACCTTACCAGGGGCCCTTGACCTTCAGCTTCGGGACCCCGACAGCAG	501
Qy	938	CTGGAACTTGAAACCGGGAGTCGGTGGCGGCACCCCAACAGAAACATCTTCGACAGTGAC	997
Db	500	CTGGGACTTGAAACCGGGAGTCGGTGGCGGCACCCCAACAGAAACATCTTCGACAGTGAC	441
Qy	998	CTGATGATAGTGCAGGCTGGGCGGCCCTTGCCGCCCCACAGCAGTAATCTGGGGCATCAGC	1057
Db	440	CTGATGATAGTGCAGGCTGGGCGGCCCTTGCCGCCCCACAGCAGTTACTCGGGCATCAGC	381
Qy	1058	GCCACGTGTACGCGACGCGGGCGCGCATGAGAGGGCGCGCGCCACCTACAGCGAGGTC	1117
Db	380	GCCACGTGTACGCGACGCGGGCGCGCATGAGAGGGCGCGCGCCACCTACAGCGAGGTC	321
Qy	1118	ATCGGCCACTACCCGGGGTCTCTCTCCAGCACACAGCAGAGCAGTGGCGGCCCTCCTTG	1177
Db	320	ATCGGCCACTACCCGGGGTCTCTCTCCAGCACACAGCAGAGCAGTGGCGGCCCTCCTTG	261
Qy	1178	CTGAGGGGACCCGGCTCCACACACACATCGGGCCCTTAGAGAGGCGAGCCTCTGG	1237
Db	260	CTGAGGGGACCCGGCTCCACACACACATCGGGCCCTTAGAGAGGCGAGCCTCTCTGG	201
Qy	1238	AGCAAGAGAGAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCGGGCT	1297
Db	200	AGCAAGAGAGAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCGGGCT	141
Qy	1298	GGGGCTGGGTAGTGAAAGGCAG	1321
Db	140	GGGGCTGGGTAGTGAAAGGCAG	117

RESULT 3

BQ641849	BQ641849	967 bp	mRNA	linear	EST 15-JUL-2002
LOCUS	AGENCOURT_8287174	NIH_MGC_43 Homo sapiens	cdna clone IMAGE:6292265		
DEFINITION	5'. mRNA sequence.				

B0641849
 B0641849.1 GI:21766021
 EST.
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Chordata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 967)
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.

high quality sequence stop: 311.

FEATURES Location/Qualifiers

 source 1..967

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/tissue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_43"
/notes="Organ: eye; Vector: pOTB7; Site: 1: XhoI; Site: 2: EcoRI; CDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI library using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong

```

in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH MGC Library. | "


```

Db      481  ACCTGCTACGGCAGCGCGGGCGCATGGAGGGGCGCGCCACCTACAGCGAGGTCAATC 540
QY      1121  GGCACACTACCGGGGCTCTCTTCCAGCACAGACAGACAGTGGGCGCCCTCTTGGTG 1180
Db      541  GGCACACTACCGGGGCTCTCTTCCAGCACAGACAGACAGTGGGCGCCCTCTTGGTG 600
QY      1181  GAGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGC 1240
Db      601  GAGGGGACCCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGC 660
QY      1241  AAGAGAGAGGATAACAGAAAGGACACCTCTTAGGGTCCCGAGGGGGCGCGGCTGGG 1300
Db      661  AAGAGAGAGGATAACAGAAAGGACACCTCTTAGGGTCCCGAGGGGGCGCGGCTGGG 720
QY      1301  GCTGCTAGGTGAAAAGGCAG 1321
Db      721  GCTGCTAGGTGAAGAGCAG 741

```

```

RESULT 7
BQ954555
LOCUS      8825282 lupski_sciatic_nerve Homo sapiens cDNA clone
DEFINITION IMAGE:6204609 5', mRNA sequence.
ACCESSION BQ954555
VERSION    BQ954555.1 GI:22370033
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens

```

```

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE
AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL   Unpublished (1999)
COMMENT   Contact: Robert Strausberg, Ph.D.

```

```

Email: cspbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

```

```

Plate: LLAM13626 row: c column: 10
High quality sequence stop: 669.

```

```

FEATURES
source

```

```

1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupski_sciatic nerve"
/notes="Vector: pCMV-SPORT6 (Life Technologies); Site 1:
NotI; Site 2: SalI; cDNA made by oligo-dT priming.
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGCTCCG-3' and
5'-GACTAGTTCTAGATCCGAGCGCCCTCT(15)-3'. Size selected >
1 kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."

```

```

ORIGIN

```

```

Query Match      55.7%; Score 736.4; DB 5; Length 916;
Best Local Similarity 95.7%; Pred. No. 5.5e-127;
Matches 800; Conservative 0; Mismatches 31; Indels 5; Gaps 4;

```

```

QY      344  GCGCGGCGGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 403
Db      1    GCGCGGCGGAGCGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCC 60
QY      404  GCGCGGCTCATGACACCGCTTGATGGGGGTCAACAGACACCGCGCGCGCGCGCGCGCGCG 463
Db      61  GCGCGGCTCATGACACCGCTTGATGGGGGTCAACAGACACCGCGCGCGCGCGCGCGCGCG 120
QY      464  CCACATGTTCTCTGACAGTGAACAAAGCTCTTTTTCAGAGCATGGAGATCACG 523
Db      121  CCACATGTTCTCTGACAGTGAACAAAGCTCTTTTTCAGAGCATGGAGATCACG 180
QY      524  GACCTGGAGTTGTTTCAGATCATCATCGTGGTGGTGTGATGATGATGATGATGATGATG 583
Db      181  GACCTGGAGTTGTTTCAGATCATCATCGTGGTGGTGTGATGATGATGATGATGATGATG 240
QY      584  ATCAGCTGCTGCTGAGCCACTACAGCTGTCTGACACGGTCTCTTTCATCAGCGGACAGC 643
Db      241  ATCAGCTGCTGCTGAGCCACTACAGCTGTCTGACACGGTCTCTTTCATCAGCGGACAGC 300
QY      644  CAGGGCGGAGAGAGAGATGCTCTCTCAGAGAGATGCTGTGGCCCTTCGGAGAGC 703
Db      301  CAGGGCGGAGAGAGAGATGCTCTCTCAGAGAGATGCTGTGGCCCTTCGGAGAGC 360
QY      704  ACAGTGTCAAGGCAACGGAATCCAGAGCGCAGGTCTACGCGCGCGCGCGCGCGCGCGCG 763
Db      361  ACAGTGTCAAGGCAACGGAATCCAGAGCGCAGGTCTACGCGCGCGCGCGCGCGCGCGCG 420
QY      764  CGCTGGCGCTGCCCGCTTTCGCGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTAT 823
Db      421  CGCTGGCGCTGCCCGCTTTCGCGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTAT 480
QY      824  CCGTACCTGCAGCAGAGATGCACTGCGACCCACCATCTCGCTGTGACAGCGGAGAG 883
Db      481  CCGTACCTGCAGCAGAGATGCACTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 540
QY      884  CCCCCACCTTACAGGCGCGCGCTGCGACCTTCCAGCTTTCGGGACCGCGAGCAGCGTGGAA 943
Db      541  CCCCCACCTTACAGGCGCGCGCTGCGACCTTCCAGCTTTCGGGACCGCGAGCAGCGTGGAA 600
QY      944  CTGAACCGGGAGTGGTGGCGGCGACCCCAACAGAACATCTTCGACAGTGAACCTGATG 1003
Db      601  CTGAACCGGGAGTGGTGGCGGCGACCCCAACAGAACATCTTCGACAGTGAACCTGATG 660
QY      1004  GATAGTGCC-AGGCTGGGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1061
Db      661  GATAGTGCCAGGCTGGGCGCGCGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 720
QY      1062  CGTGTCTACGCGCAGCGCGCGCG-GCATGGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1120
Db      721  CGTGTCTACGCGCAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 780
QY      1121  GGCCTA-CTACCGCGGCTCTCTCTTCAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1174
Db      781  GGCCTA-CTACCGCGGCGCGCGCTCTCTTCACCGCGCGCGCGCGCGCGCGCGCGCGCGCG 836

```

```

RESULT 8

```

```

AL558881/c

```

```

LOCUS

```

```

DEFINITION

```

```

ACCESSION

```

```

VERSION

```

```

KEYWORDS

```

```

SOURCE

```

```

ORGANISM

```

```

REFERENCE

```

```

AUTHORS

```

```

TITLE

```

```

AL558881      850 bp      mRNA      linear      EST 02-APR-2004
Homo sapiens cDNA clone CS0DJ015YF12 3-PRIME, mRNA sequence.
AL558881
EST.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 850)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization

```



```

Db 747 ATGCTTGTGGCCYTCGGAGAGACAGTGTCTAGGCAACGAAATCCAGAGCCGCA-GTYTA 689
Qy 742 CCCCCCGCTCGGCCACCGACCGCTCGCGCTGCGGCTTTCGCCACGAGCGGAGCGTT 801
Db 688 CGCCCGCTTCGGCCACCGACCGCTGCGGCTGCGGCTTTCGCCACGAGCGGAGCGTT 629
Qy 802 CCACCGCTTCAGGCCACCTATTCGTAACCTTCAGACGAGATCGACCTGCGCCACCCAT 861
Db 628 CCACCGCTTCAGGCCACCTATTCGTAACCTTCAGACGAGATCGACCTGCGCCACCCAT 569
Qy 862 CTCGCTGTACAGCGGAGGAGCCCGACCTACAGGCGCCCTGCACTTCAGCTTCG 921
Db 568 CTCGCTGTACAGCGGAGGAGCCCGACCTACAGGCGCCCTGCACTTCAGCTTCG 509
Qy 922 GGACCCCGAGCAGCTGGAACCTGAAACCGGAGTTCGCTGCGCGCACCCCAACAGAAC 981
Db 508 GGACCCCGAGCAGCTGGAACCTGAAACCGGAGTTCGCTGCGCGCACCCCAACAGAAC 449
Qy 982 CATCTTCAGACGTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 1041
Db 448 CATCTTCAGACGTGACCTGATGATGATGATGATGATGATGATGATGATGATGAT 389
Qy 1042 TAACTTCGGGATCAGCGCAGCTGCTAGCGGAGTTCGCTGCGCGCACCCCAACAGAAC 1101
Db 388 TAACTTCGGGATCAGCGCAGCTGCTAGCGGAGTTCGCTGCGCGCACCCCAACAGAAC 329
Qy 1102 CACTACAGCAGGTCTATCGGCCACTACCGGGGCTCTCTTCAGCAGCAGCAGCAGCAG 1161
Db 328 CACTACAGCAGGTCTATCGGCCACTACCGGGGCTCTCTTCAGCAGCAGCAGCAGCAG 269
Qy 1162 TGGGCGGCGCTCTCTGCTGAGGGGACCGGCTCCACACACACACACACACACACAC 1221
Db 268 TGGGCGGCGCTCTCTGCTGAGGGGACCGGCTCCACACACACACACACACACACAC 209
Qy 1222 GAGCGCAGCATCTGGAGCAAGAGAGAGATTAACAGAAAGGACACCTCTCTAGGGTCC 1281
Db 208 GAGCGCAGCATCTGGAGCAAGAGAGAGATTAACAGAAAGGACACCTCTCTAGGGTCC 149
Qy 1282 CCAGGGGGCGGCGCTGCGGCTGCTAGGTGAAAGGAG 1321
Db 148 CCAGGGGGCGGCGCTGCGGCTGCTAGGTGAAAGGAG 109

RESULT 10
AL558882 897 bp mRNA linear EST 02-APR-2004
LOCUS AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
DEFINITION Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.
ACCESSION AL558882
VERSION AL558882.3 GI:46184269
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 897)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:31283015.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06QP1&c=9945.r.
Location/Qualifiers

```

FEATURES

source

```

1. .897
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/cell_line="JURKAT"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
10-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

```

ORIGIN

```

Query Match 54.1%; Score 714.6; DB 1; Length 897;
Best Local Similarity 99.3%; Pred. No. 6.3e-123;
Matches 736; Conservative 2; Mismatches 1; Indels 2; Gaps 2;

Qy 581 GTGATCAGCTGCTGCTGAGCCACTACAAGTCTCTGCAAGGTCCTTTCATCAGCCGCGAC 640
Db 1 GTGATCAGCTGCTGCTGAGCCACTACAAGTCTCTGCAAGGTCCTTTCATCAGCCGCGAC 60
Qy 641 AGCCAGGGGCGAGGAGAGAGATGCCCTGTCTCTAGAAAGGATGCTGTGGCCCTCGGAG 700
Db 61 AGCCAGGGGCGAGGAGAGAGATGCCCTGTCTCTAGAAAGGATGCTGTGGCCCTCGGAG 120
Qy 701 AGCACAGTGTCAAGCAACGGAATCCAGAGCGCAGTCTACGCCCGGCTCGGCCAC 760
Db 121 AGCACAGTGTCAAGCAACGGAATCCAGAGCGCAGTCTACGCCCGGCTCGGCCAC 179
Qy 761 GACCGCTGCGCGCTGCGCGCTTCGCCCGAGCGGAGCGCTTCACCGCTTCAGAGCCAC 820
Db 180 GACCGCTGCGCGCTGCGCGCTTCGCCCGAGGGAGCGCTTCACCGCTTCAGAGCCAC 239
Qy 821 TATCCGTACTGACGACGACGATCGACCTGCGACCCACCAATCTCGTGTGACAGGGGAG 880
Db 240 TATCCGTACTGACGACGATCGACCTGCGCGCCACCAATCTCGTGTGACAGGGGAG 299
Qy 881 GAGCCCGCCACCTTACCAGGGCGCTGCACTCCAGCTTCGGGAGCCCGGAGCAGAGCTG 940
Db 300 GAGCCCGCCACCTTACCAGGGCGCTGCACTTCAGCTTCGGGAGCCCGGAGCAGAGCTG 359
Qy 941 GAACTGAACCGGGAGTTCGCTGCGCGCACCCCAACAGAACCACTTTCGACAGTGCACCTG 1000
Db 360 GAACTGAACCGGGAGTTCGCTGCGCGCACCCCAACAGAACCACTTTCGACAGTGCACCTG 419
Qy 1001 ATGATAGTGCAGAGCTGGGCGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1060
Db 420 ATGATAGTGCAGAGCTGGGCGGCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 479
Qy 1061 AGCTGTACGCGCGCGCGCGCGCATGGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 1120
Db 480 AGCTGTACGCGCGCGCGCGCGCATGGAGGGCGCGCGCGCGCGCGCGCGCGCGCGCG 539
Qy 1121 GGCCTACTACCGGGGTCCTCTTCCAGACACCAAGAGAGAGAGTGGGCGCGCGCTTCCTG 1180
Db 540 GGCCTACTACCGGGGTCCTCTTCCAGACACCAAGAGAGAGAGTGGGCGCGCGCTTCCTG 599
Qy 1181 GAGGGGACCGGCTCCACACACACATCGCGCGCGCTTAGAGAGCGCAGCCTTCGAGC 1240
Db 600 GAGGGGACCGGCTCCACACACACATCGCGCGCGCTTAGAGAGCGCAGCCTTCGAGC 658
Qy 1241 AAAGAGAGAGATTAACAGAAAGGAGACCTCTCTTAGGGTCCCGAGGGGGCGCGCGTGG 1300
Db 659 AAAGAGAGAGATTAACAGAAAGGAGACCTCTCTTAGGGTCCCGAGGGGGCGCGCGTGG 718
Qy 1301 GCTCGTGTAGGTGAAAGGAG 1321
Db 719 GCTCGTGTAGGTGAAAGGAG 739

```

RESULT 11

BUS39219
LOCUS BUS39219 945 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT_10215265 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6569922 5', mRNA sequence.
ACCESSION BUS39219
VERSION BUS39219.1 GI:22849660
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 945)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2757 row: p column: 18
High quality sequence stop: 663.
Location/Qualifiers
1. .945
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6569922"
/issue_type="adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 107"
/note="Organ: breast; Vector: pOTB7; Site: 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 52.3%; Score 691.2; DB 5; Length 945;
Best Local Similarity 93.7%; Pred.No.1.4e-118;
Matches 764; Conservative 0; Mismatches 44; Indels 7; Gaps 4;
QY 499 TTGTGTTCCAGAGCATGCGAGTCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 558
DB 65 TCTCTCGGAACACGAGCAATGCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 124
QY 559 GGTGATGATGGTATGGTGTGTGATCAGTCGCTGCTGAGCCACTACAGCTGTCTGC 618
DB 125 GGTGATGATGGTGTGTGTGATCAGTCGCTGCTGAGCCACTACAGCTGTCTGC 184
QY 619 ACGGTCTTCATCAGCGGCACAGCAGCGGCGGAGAGAGATGCCCTGTCTCAGA 678
DB 185 ACGGTCTTCATCAGCTGGGCACAGCCAGCGGCGGAGAGAGATGCCCTGTCTCAGA 244
QY 679 AGGATGCTGTGGCCCTCGGAGAGCAGTGTTCAGCAACGGAATCCAGAGCGCGAGT 738
DB 245 AGGATGCTGTGGCCCTCGGAGAGCAGTGTTCAGCAACGGAATCCAGAGCGCGAGT 304
QY 739 CTAGCGCCCGCTCGGCCCAACGACCGCTGGCCGCTTGGCCCGAGCGGAGCG 798
DB 305 CTAGCGCCCGCTCGGCCCAACGACCGCTGGCCGCTTGGCCCGAGCGGAGCG 364
QY 799 CTTCCACCGCTTCAGCGCCACCTATCGGTACCTGCGACGAGATGCAGCTGCCACCCAC 858
DB 365 CTTCCACCGCTTCAGCGCCACCTATCGGTACCTGCGACGAGATGCAGCTGCCCGCCAC 424

QY 859 CATCTCGCTGTACAGCGGGAGAGCCGCCACCTACCAAGGGCCCTTGACACCTCCAGCT 918
DB 425 CATCTCGCTGTGAGCGGGAGAGAGCCGCCACCTACCAAGGGCCCTTGACACCTCCAGCT 484
QY 919 TCGGAGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCTGGTGGCGGCACCCCAACAG 978
DB 485 TCGGAGACCCCGAGCAGCAGCTGGAACTGAACCGGGAGTCTGGTGGCGGCACCCCAACAG 544
QY 979 AACCATCTTCGACAGTGAAGCTGATGATAGTGCAGGCTGGGGCGGCCCTTGCCCGCCAG 1038
DB 545 AACCATCTTCGACAGTGAAGCTGATGATAGTGCAGGCTGGGGCGGCCCTTGCCCGCCAG 604
QY 1039 CAGTAACTCGGGCATCAGCGCCACGCTGCTACCGCAGCGGGCGGCATGAGAGGGCGGCC 1098
DB 605 CAGTAACTCGGGCATCAGCGCCACGCTGCTACCGCAGCGGGCGGCATGAGAGGGCGGCC 664
QY 1099 GCCCACTACAGCGAGGTCTATCGGCCATCTACCGGGGTCTCTCTTCAGCACCAGAGAG 1158
DB 665 GCCCACTACAGCGAGGTCTATCGGCCATCTACCGGGGTCTCTCTTCAGCACCAGAGAG 724
QY 1159 CAGTGGCGGCCCT-CTTTCTGGAGGGGACCCGGCTCCACCAACACACATCGCG-CCC 1216
DB 725 CAGTGGCGGCCCTCTCTTTGCTGGAGGGGACCCGGCTCCACCAACACACATCGTGCCCC 784
QY 1217 CTAGAGAGCGCAG-CCATCTGGAGCAAGAGAGAGTAA- ----CAGAAAGACACCTC 1271
DB 785 CTAAGAGCGCAGCCATCTGGAGCAAGAGAGTAAACCCGAAAGGACACCTTC 844
QY 1272 TCTAGGGTCCCGAGGGGGCGGGCTGGGGCTGCG 1306
DB 845 TTCTAGGTCCCCCGAGGGGGCGGGCGCGCTGGG 879
RESULT 12
LOCUS BUS39219
DEFINITION AGENCOURT_10016502 NIH_MGC_142 Homo sapiens cDNA clone
IMAGE:6497853 5', mRNA sequence.
ACCESSION BUS39219
VERSION BUS39219.1 GI:23254677
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 850)
AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: NCI
CDNA Library Preparation: Michael Brownstein Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLCM2679 row: i column: 22
High quality sequence stop: 499.
Location/Qualifiers
1. .850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6497853"
/issue_type="mixed (pool of 40 RNAs)"
/lab_host="DH10B (T1-phage-resistant)"
/clone_lib="NIH MGC 142"
/note="Vector: pDNR-LIB; Site 1: SfiI (ggcattatggc);
Site 2: SfiI (ggccctccggc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -

[illegible]

RESULT 15	
BC023092	
LOCUS	
DEFINITION	BC023092 1079 bp mRNA linear HTC 20-SEP-2002 Mus musculus, Nedd4 WW binding protein 4, clone IMAGE:3989996, tRNA.
ACCESSION	BC023092
VERSION	BC023092.1 GI:18605637
KEYWORDS	HTC.
SOURCE	Mus musculus (house mouse)
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
AUTHORS	1 (bases 1 to 1079) Strausberg,R.
TITLE	Direct Submission

QY	837	ACGAGATCGACCTGCGCACCCACCATCTCGCTGTGACACGGGAGGAGCCCCACCCCTACC	896
Db	423	ACGAAATGCGCTGCGCACCCACCATCTCACTGTCTGATGGGGAGGAGCCCCACCCCTACC	482
QY	897	AGGGCCCTTGACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAAACCGGAGT	956
Db	483	AGGGCCCTTGACCCCTCCAGCTAGGGGACCCCTGAGCAACAGCTGGAGCTGAACCGGGAAT	542
QY	957	CGGTGCGCGACCCCAACAGAAACATCTTCGACAGTGACCTGTGATGGATAGTGCCAGGC	1016
Db	543	CTGTGCGCGACCCCTTAACCGGACCATCTTCGACAGTGACCTTATAGACAGCACCATGC	602
QY	1017	TGGGCGGCGCCCTGCGCCCGCCGACGTAACTCGGGGCATCAGCGCCAGTGTCTACGCGAGCG	1076
Db	603	TGGGGGGGGCCCTGTCCCGCCGACGAGTAACCTCGGGGCATCAGCGCCAGTGTCTACGCGAGCG	662
QY	1077	GCGGGGCGCATGGAGGGGCGCGCCGCCACCTACAGCGAGGTCACTCGGCCACTACCGGGGT	1136
Db	663	GTGGGGCGCATGGAGGGGCGCGCCGCCACCTACAGCGAGGTCACTCGGCCACTACCGTGGCT	722
QY	1137	CCTCCTTCCAGCACACGACAGCAGAGCAGTGGGCGCGCCCTCCTTGTGTGGAGGGAGCCCGGCTCC	1196
Db	723	CCTCCTTCCAGCACACGACAGCAGTGGGCGCGCCCTCCTTGTGTGGAGGGAGCCCGGCTCC	782
QY	1197	ACCACACACATCGCGCCCGCTAGAGAGCGCGCCCATCTGGAGCAAGAGAGGATAAAC	1256
Db	783	ATCACTCGCACATTGCCCCCACTGGA-----GAAACAAGGAGAGGAGAAAC	827
QY	1257	AGAAAGGACACCCCTCTCTAGGGTCCCGAGGGGGGCGG	1293
Db	828	AGAAAGGTCAACCCCTCTAGGAGTGGGGGCGCGGGCG	864

Search completed: February 19, 2005, 16:15:48
Job time : 4163.31 secs

This Page Blank (usp10)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 16:23:01 ; Search time 5698.7 Seconds
(without alignments)
11232.262 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcggtctcgagagcga.....ctgcgttagtgaaaggcag 1321

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 4708233 seqs, 24227607955 residues

Word size : 0

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba.*
2: gb_hgt.*
3: gb_in.*
4: gb_cm.*
5: gb_ov.*
6: gb_pat.*
7: gb_ph.*
8: gb_pl.*
9: gb_pr.*
10: gb_ro.*
11: gb_sts.*
12: gb_sy.*
13: gb_un.*
14: gb_vi.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1321	100.0	1321	6	AX392417	Sequence
2	1229	93.0	4839	6	CQ812357	Sequence
3	1229	93.0	4839	9	AF305616	Homo sapi
4	1178	89.2	1303	6	AX775889	Sequence
5	861	65.2	861	6	AX392419	Sequence
6	838	63.4	1061	9	BC015918	Homo sapi
7	800	60.6	1140	6	AR336830	Sequence
8	800	60.6	1141	9	AF224278	Homo sapi
9	800	60.6	1818	9	AY128643	Homo sapi
10	755	57.2	759	6	AR336831	Sequence
11	749	56.7	969	6	BD272494	Secreted
12	749	56.7	1085	6	AX775887	Sequence
13	749	56.7	1913	6	BD272544	Secreted
14	744	56.3	969	6	BD272514	Secreted
15	704	53.3	759	6	BD272545	Secreted
16	701	53.1	753	6	BD272534	Secreted
17	701	53.1	756	6	BD272495	Secreted
18	698	52.8	969	6	BD272515	Secreted
19	698	52.8	969	6	BD272516	Secreted

20	647	49.0	1060	9	BC080635	Homo sapi
21	600	45.4	600	6	CQ728942	Sequence
22	593	44.9	61505	9	AF305426	Homo sapi
c 23	593	44.9	130435	9	HS71807	Human DNA
c 24	560	42.4	1583	6	AX593655	Sequence
c 25	521	39.4	150224	9	HSJ1059L7	Human DNA
c 26	401	30.4	408	6	AX071267	Sequence
c 27	302	22.9	693	6	AX392430	Sequence
28	271	20.5	812	6	BD226320	Pancreat
29	271	20.5	812	6	AX011709	Sequence
30	110	8.3	270	6	CQ735730	Sequence
31	60	4.5	60	6	CQ543985	Sequence
32	51	3.9	51	6	AX199565	Sequence
33	44	3.3	411	6	BD272547	Secreted
34	44	3.3	484	6	BD272546	Secreted
35	44	3.3	648	6	BD272535	Secreted
36	44	3.3	651	6	BD272505	Secreted
37	44	3.3	651	10	AF220208	Mus muscu
38	44	3.3	878	6	AX392428	Sequence
39	44	3.3	895	10	BC069890	Mus muscu
40	44	3.3	1265	5	AJ720618	Gallus ga
41	44	3.3	1379	10	BC036995	Mus muscu
42	44	3.3	1713	6	BD272504	Secreted
43	44	3.3	1713	6	BD272517	Secreted
44	44	3.3	1713	6	BD272518	Secreted
45	44	3.3	1713	6	BD272519	Secreted

ALIGNMENTS

RESULT 1	AX392417	AX392417	1321 bp	DNA	linear	PAT 23-MAR-2002
LOCUS	Sequence 1	from Patent WO0216416				
DEFINITION	AX392417					
ACCESSION	AX392417.1	GI:19700732				
VERSION						
KEYWORDS						
SOURCE	Homo sapiens (human)					
ORGANISM	Homo sapiens					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.					
REFERENCE	Lee, R.T., Landschulz, K.T., Kennedy, S.P., Thompson, J.F. and Turi, T.G.					
AUTHORS	Diagnosis and treatment of cardiovascular conditions					
TITLE	Patent: WO 0216416-A 1 28-FEB-2002;					
JOURNAL	THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)					
FEATURES	Location/Qualifiers					
source	1. .1321					
	/organism="Homo sapiens"					
	/mol_type="unassigned DNA"					
	/db_xref="taxon:9606"					
	413_1276					
	/note="unassigned protein product"					
	/codon_start=1					
	/protein_id="CAD29005.1"					
	/db_xref="GI:19700732"					
	/translation="MRLMGNVSTAAAGQPNVCTCKKSLFOSMEITELEFVQI					
	IIIVVMVVMVITCLASHYKLSARSFHSRQRRDALSGCLWPSESTVSGN					
	GIPEQVAPPPPTDLRVLPPAQRFRFRFQPTLYLQHEIDLPTTISLDEEPPPP					
	YQSGCTQLRDPEQLNRSVRAPPNTIFDSDLMDSARGLGCPFPSSNSGISATC					
	YQSGRMGEPPPTSEVIGHYFGSSFHQOQSSGPPSLLEGTRLHHTHIAPLSAAIWS					
	KEKDKQKGHPL"					

ORIGIN

Query Match	100.0%;	Score 1321;	DB 6;	Length 1321;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 1321;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	CGACCGCGTCTCGGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGCG	60	
Db	1	CGACCGCGTCTCGGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGCG	60	


```
QY 633 GCCGGCAGCCAGCGGCGGAGAGAGATGCTCTGTCTCTCAGAGGATGCTGTGGC 692
Db 541 GCCGGCAGCCAGCGGCGGAGAGAGATGCTCTGTCTCTCAGAGGATGCTGTGGC 600
QY 693 CTTGGAGAGACAGTGTACGAGCAACGAAATCCAGAGCGGAGTGTACGCCCGGCTC 752
Db 601 CTTGGAGAGACAGTGTACGAGCAACGAAATCCAGAGCGGAGTGTACGCCCGGCTC 660
QY 753 GGCCACCGACCGCTGGCGGCTGCGCCCTTCCGCCAGCGGAGCGCTTCCACGGCTTC 812
Db 661 GGCCACCGACCGCTGGCGGCTGCGCCCTTCCGCCAGCGGAGCGCTTCCACGGCTTC 720
QY 813 AGCCACCTATCTCGTACCTGACGACAGAGATGCACTGCGCCACCCAGCATCTCGCTGTAG 872
Db 721 AGCCACCTATCTCGTACCTGACGACAGAGATGCACTGCGCCACCCAGCATCTCGCTGTAG 780
QY 873 ACGGAGAGAGCCCGACCTTACAGGCGCCCTTGCACCTTCCAGCTTCCGGAACCCGAGC 932
Db 781 ACGGAGAGAGCCCGACCTTACAGGCGCCCTTGCACCTTCCAGCTTCCGGAACCCGAGC 840
QY 933 AGCAGCTGGAACCTGAACCGGAGTCCGCTGCGCGCACCCCGACAGAACCATCTTCGACA 992
Db 841 AGCAGCTGGAACCTGAACCGGAGTCCGCTGCGCGCACCCCGACAGAACCATCTTCGACA 900
QY 993 GTGACCTGTAGTGTAGTGGCGGCGGCGCCCTTGCACCTTCCAGCAGTAACTCGGGCA 1052
Db 901 GTGACCTGTAGTGTAGTGGCGGCGGCGCCCTTGCACCTTCCAGCAGTAACTCGGGCA 960
QY 1053 TCAGCGCAGCTGTACGAGAGCGGCGGCGGAGTGAAGAGGCGCGCCCGCCAGCTTACAGCG 1112
Db 961 TCAGCGCAGCTGTACGAGAGCGGCGGCGGAGTGAAGAGGCGCGCCCGCCAGCTTACAGCG 1020
QY 1113 AGGTCTCGGCACTACCGGGGTCTCTTCCAGCAGCAGCAGAGTGGCGGCGCCCT 1172
Db 1021 AGGTCTCGGCACTACCGGGGTCTCTTCCAGCAGCAGCAGAGTGGCGGCGCCCT 1080
QY 1173 CTTGTGTAGAGGAGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA 1232
Db 1081 CTTGTGTAGAGGAGACCGGCTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCA 1140
QY 1233 TCTGAGCAAGAGAGAGTAAACAGAAAGGACACCTCTTAGGTGCTCCAGGGGGGC 1292
Db 1141 TCTGAGCAAGAGAGAGTAAACAGAAAGGACACCTCTTAGGTGCTCCAGGGGGGC 1200
QY 1293 GGGCTGGGCTGCTAGGTGAAGGACAG 1321
Db 1201 GGGCTGGGCTGCTAGGTGAAGGACAG 1229
```

```
RESULT 4
AX775889 1383 bp mRNA linear PAT 14-JUL-2003
LOCUS AX775889
DEFINITION Sequence 159 from Patent WO03048202.
ACCESSION AX775889
VERSION AX775889.1 GI:32693607
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Matsuda,A. and Muramatsu,S.
TITLE NF-kB activating gene
JOURNAL Patent: WO 03048202-A 159 12-JUN-2003;
Asahi Kasei Kabushiki Kaisha (JP)
FEATURES
Location/Qualifiers
source 1. .1383
/mol_type="mRNA"
/db_xref="taxon:9606"
321. .1184
/note="unnamed protein product"
```

```
/codon_start=1
/protein_id="CAE11644.1"
/db_xref="GI:32693608"
/translation="MRLMGVNSTAAARAGQNVSCCTCNKBSLPSOMTELEFVQI
IIIVVMVWVITCLSHYKLSARSFIRSHQRRRDLALSSGCLMPSLSTVSGN
GIPEQVYAPPRPTDLRAVFPQARFRFQTPYLOHEIDLPSLSDGEEPP
YQPCPTQLRDEPQLELNRESVRAPPNRTIFDSDLMARSALGGPCPPSSNGISATC
YSGGRMEGPPPTYSVIVGHYPGSPFHQOQSGPPSLLEGTRLHHTHIAPLSAAIWS
KEKQKQKHPL"
ORIGIN
Query Match 89.2%; Score 1178; DB 6; Length 1383;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 93 GGAAGCTAGCGGAGAGGCTCAGCCCCGGCGGAGCGCGCCCGCTGCCAGGCCATT 152
Db 1 GGAAGCTAGCGGAGAGGCTCAGCCCCGGCGGAGCGCGCCCGCTGCCAGGCCATT 60
QY 153 TTCCGAGACGCCACCCGCGGCGACTGCGGACGCCCCCGGGCTGCGAGGGAGCGCGGG 212
Db 61 TTCCGAGACGCCACCCGCGGCGACTGCGGACGCCCCCGGGCTGCGAGGGAGCGCGGG 120
QY 213 GGGCGCAGCGGAGCGGCTCCCGGCACTGAGCCCCCGCGGCGCCCGGGAACATTGCGGC 272
Db 121 GGGCGCAGCGGAGCGGCTCCCGGCACTGAGCCCCCGCGGCGCCCGGGAACATTGCGGC 180
QY 273 GACCCGAGCCCGGCGGAGCGGCGGCGCTCCCGCGCGCGGCGCTTCTGCAATGCGGGGC 332
Db 181 GACCCGAGCCCGGCGGAGCGGCGGCGCTTCCCGCGCGCGGCGCTTCTGCAATGCGGGGC 240
QY 333 CCCAGCTCCGGCGCGCGGCGGAGCCCCCGCGGCGCCCGAGCCCCCGCGGCCCGCGC 392
Db 241 CCCAGCTCCGGCGCGCGGCGGAGCCCCCGCGGCGCCCGAGCCCCCGCGGCCCGCGC 300
QY 393 GCGCGCCCGCGCGCGCTCCATGACCGCTTATGGGGGTCAACAGCAACCGCGCGCGCG 452
Db 301 GCGCGCCCGCGCGCGCTCCATGACCGCTTATGGGGGTCAACAGCAACCGCGCGCGCG 360
QY 453 CGCGCGGCGAGCCCAATGCTCTCGACGTCAACTGCAAAAGCTTTGTTCAGAGCA 512
Db 361 CGCGCGGCGAGCCCAATGCTCTCGACGTCAACTGCAAAAGCTTTGTTCAGAGCA 420
QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGTGTGTGTGA 572
Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTGTGTGTGTGTGTGA 480
QY 573 TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 632
Db 481 TGGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 540
QY 633 GCGGCGACAGCGGCGGAGGAGAGATGCGCTGCTCTCAGAGGATGCTGTGTGTGTGT 692
Db 541 GCGGCGACAGCGGCGGAGGAGAGATGCGCTGCTCTCAGAGGATGCTGTGTGTGTGTGT 600
QY 693 CTTGGAGAGACAGTGTGTCAGCAACCGGAAATCCAGAGCGGAGTGTACGCCCGGCTC 752
Db 601 CTTGGAGAGACAGTGTGTCAGCAACCGGAAATCCAGAGCGGAGTGTACGCCCGGCTC 660
QY 753 GGGCCACCGACCGCTTGGCGGCTTGGCGGCGGCGGAGCGGCTTCCAGCGGTTCC 812
Db 661 GGGCCACCGACCGCTTGGCGGCTTGGCGGCGGCGGAGCGGCTTCCAGCGGTTCC 720
QY 813 AGCCACCTATCTCGTACCTGACGACAGAGATGCACTGCGCCACCCAGCATCTCGCTGTAG 872
Db 721 AGCCACCTATCTCGTACCTGACGACAGAGATGCACTGCGCCACCCAGCATCTCGCTGTAG 780
QY 873 ACGGAGAGAGCCCGACCCCTTACAGGCGCCCTTGCACCTTCCAGCTTCCGGAACCCCGAGC 932
Db 781 ACGGAGAGAGCCCGACCCCTTACAGGCGCCCTTGCACCTTCCAGCTTCCGGAACCCCGAGC 840
QY 933 AGCAGCTGGAACCTGAACCGGAGTCCGCTGCGCGCACCCCGACAGAACCATCTTCGACA 992
```


[illegible]


```
VERSION BD272544.1 GI:33082312
KEYWORDS JP 2002539773-A/53.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1913)
AUTHORS Barnes, I.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
TITLE Secreted proteins and nucleic acids encoding them
JOURNAL Patent: JP 2002539773-A 53 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002539773-A/53
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
PI FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
G01N33/15,
PC G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
Secreted proteins and nucleic acids encoding them FH Key
FT source Location/Qualifiers
FT 1.1913 /organism="Homo sapiens (human)".
FEATURES
source Location/Qualifiers
1.1913
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 56.7%; Score 749; DB 6; Length 1913;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 799; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 522 CGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTATGATGGTGGTGG 581
DB 150 CGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTATGATGGTGGTGG 209
QY 582 TGATCAGTCCCTGCTCAGCAGCCTACAGCTGTCTGACAGGATGCTGTGGCCCTCGGAGA 641
DB 210 TGATCAGTCCCTGCTCAGCAGCCTACAGCTGTCTGACAGGATGCTGTGGCCCTCGGAGA 269
QY 642 GCCAGGGGGGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGA 701
DB 270 GCCAGGGGGGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGA 329
QY 702 GCACAGTGTGAGCAACGGAATCCAGAGCGCAGGTCTACGGCCCGCTCGGCGCCACCG 761
DB 330 GCACAGTGTGAGCAACGGAATCCAGAGCGCAGGTCTACGGCCCGCTCGGCGCCACCG 389
QY 762 ACCGCTGGCGCTGGCCCTTCCGCCAGCGGGAGCGCTTCCACCGCTTCAGCCCACT 821
DB 390 ACCGCTGGCGCTGGCCCTTCCGCCAGCGGGAGCGCTTCCACCGCTTCAGCCCACT 449
QY 822 ATCGTACCTGCAGCAGAGATCGACCTGCGCCACCCACCATCTCGCTGTGAGCGGGAGG 881
DB 450 ATCGTACCTGCAGCAGAGATCGACCTGCGCCACCCACCATCTCGCTGTGAGCGGGAGG 509
QY 882 AGCCCCACCCCTACAGGGCCCCCTGCACTCCAGCTTCGGGAGCCCGCAGCAGAGCTGG 941
DB 510 AGCCCCACCCCTACAGGGCCCCCTGCACTCCAGCTTCGGGAGCCCGCAGCAGAGCTGG 569
QY 942 AACTGAACCGGAGTGGTGGGGGCAACCCCAACAGAACCATCTTCGACGAGTACCTGA 1001
DB 570 AACTGAACCGGAGTGGTGGGGGCAACCCCAACAGAACCATCTTCGACGAGTACCTGA 629
QY 1002 TGGATAGTGCAGGCTGGGGGGCCCCCTGCCCGCCAGCAGTAATCTGGGGCATCAGGCCCA 1061
DB 630 TGGATAGTGCAGGCTGGGGGGCCCCCTGCCCGCCAGCAGTAATCTGGGGCATCAGGCCCA 689
QY 1062 CGTGCTACGGCAGCGGGGCGATGGAGGGGGCGCGCGCCCACTACAGCGAGGTCTATCG 1121
```

```
DB 690 CGTGCTACGGCAGCGGGCGCATGAGGGGGCGCGCCCACTACAGGAGTCTATCG 749
QY 1122 GCCACTACCGGGGTCTCTCTCCAGCACCAGCAGAGCAGTGGGCGCCCTCTCTTGTGG 1181
DB 750 GCCACTACCGGGGTCTCTCTCCAGCACCAGCAGAGCAGTGGGCGCCCTCTCTTGTGG 809
QY 1182 AGGGGACCGGGCTCCACACACACATCGCGCCCTTAGAGAGGCGAGCCATCTGGAGCA 1241
DB 810 AGGGGACCGGGCTCCACACACACATCGCGCCCTTAGAGAGGCGAGCCATCTGGAGCA 869
QY 1242 AACAGAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCGGGCTGGG 1301
DB 870 AACAGAGGATAAACAGAAAGGACACCTCTCTAGGGTCCCCAGGGGGCGGGCTGGG 929
QY 1302 CTGCTAGGTGAAAGGCAG 1321
DB 930 CTGCTAGGTGAAAGGCAG 949
RESULT 14
BD272514
LOCUS BD272514 969 bp DNA linear PAT 17-JUL-2003
DEFINITION Secreted proteins and nucleic acids encoding them.
ACCESSION BD272514
VERSION BD272514.1 GI:33082282
KEYWORDS JP 2002539773-A/23.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 969)
AUTHORS Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.
TITLE Secreted proteins and nucleic acids encoding them
JOURNAL Patent: JP 2002539773-A 23 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002539773-A/23
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C
PI FRASER
PC C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC
G01N33/15,
PC G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC
Secreted proteins and nucleic acids encoding them FH Key
FT CDS Location/Qualifiers
(6)..(761).
FEATURES
source Location/Qualifiers
1..969
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 56.3%; Score 744; DB 6; Length 969;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 794; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 527 CTGAGTTGTTTCAGATCATCATCTCGTGGTGGTATGATGATGATGATGATGATGATC 586
DB 15 CTGAGTTGTTTCAGATCATCATCTCGTGGTGGTATGATGATGATGATGATGATGATC 74
QY 587 ACCTGCTGCTGAGCCACTACAGCTGTCTGACGGTCTCTTCATCAGCGGACAGCCAG 646
DB 75 ACCTGCTGCTGAGCCACTACAGCTGTCTGACGGTCTCTTCATCAGCGGACAGCCAG 134
QY 647 GGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGAGCACA 706
DB 135 GGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGAGCACA 194
QY 707 GTGTCAGGCAACGAATCCAGAGCGCGAGGTCTACGCCCGGCTCGGCCACCGCCG 766
```

```
Db 195 GTGTGAGCAACGAATCCAGAGCCGAGGTCTACGCCCGCCCTCGGCCACCGACCGC 254
Qy 767 GTGCGGTGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 826
Db 255 CTGCGCGTGCCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 314
Qy 827 TACCTGACGACGAGATCGACTCGCTGCCACCCACCACTCTCGCTGTGTCAGACGGGAGGAGCCC 886
Db 315 TACCTGACGACGAGATCGACTCGCTGCCACCCACCACTCTCGCTGTGTCAGACGGGAGGAGCCC 374
Qy 887 CCACCTTACGAGGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 946
Db 375 CCACCTTACGAGGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 434
Qy 947 AACCGGAGTGGGTGCGCGACCCCAACAGAACCACTTTCGACAGTGCCTGATGGAT 1006
Db 435 AACCGGAGTGGGTGCGCGACCCCAACAGAACCACTTTCGACAGTGCCTGATGGAT 494
Qy 1007 AGTCCAGGTTGGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 1066
Db 495 AGTCCAGGTTGGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 554
Qy 1067 TACCGGAGCGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 1126
Db 555 TACCGGAGCGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 614
Qy 1127 TACCGGAGCGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 1186
Db 615 TACCGGAGCGCGCGCTTTCGCCGACGCGGAGCGCTTCCACCGCTTCCAGCGCCACCTATCCG 674
Qy 1187 ACCCGGTTCCACCAACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGAGCAAAAGAG 1246
Db 675 ACCCGGTTCCACCAACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGAGCAAAAGAG 734
Qy 1247 AAGGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGGCGCGGGTGGGGTGGCG 1306
Db 735 AAGGATTAACAGAAAGACACCTCTCTAGGGTCCCGAGGGGCGCGGGTGGGGTGGCG 794
Qy 1307 TAGGTGAAAAGGCGAG 1321
Db 795 TAGGTGAAAAGGCGAG 809

RESULT 15
BD272545
LOCUS Secreted proteins and nucleic acids encoding them.
DEFINITION 759 bp DNA linear PAT 17-JUL-2003
ACCESSION BD272545
VERSION BD272545.1 GI:33082313
KEYWORDS JP 2002539773-A/54.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 759)
Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
Secreted proteins and nucleic acids encoding them
Patent: JP 2002539773-A 54 26-NOV-2002;
MILLENNIUM PHARMACEUTICALS INC
OS Homo sapiens (human)
PN JP 2002539773-A/54
PD 26-NOV-2002
PF 01-MAR-2000 JP 2000602247
PR 01-MAR-1999 US 60/122458
PI THOMAS M BARNES,DOUGLAS A HOLTZMAN,JOHN D SHARP,CHRISTOPHER C
PI FRASER
PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68,PC
GOIN33/15,
PC GOIN33/50,GOIN33/53,GOIN33/56,GOIN33/566,C12N15/00,C12N5/00,CC
Secreted proteins and nucleic acids encoding them FH Key
Location/Qualifiers
FT source 1..759
```

/organism='Homo sapiens (human)'

Location/Qualifiers

1..759

/organism='Homo sapiens'

/mol_type='genomic DNA'

/db_xref='taxon:9606'

ORIGIN

Query Match 53.3%; Score 704; DB 6; Length 759;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 754; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 522 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGAATGGTGAATGGTGG 581

Db 5 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGAATGGTGAATGGTGG 64

Qy 582 TGATCATGCTGCTGTGAGCCACTACAAGTGTCTGACGGTCTTTCATCAGCGGACCA 641

Db 65 TGATCATGCTGCTGTGAGCCACTACAAGTGTCTGACGGTCTTTCATCAGCGGACCA 124

Qy 642 GCCAGGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGTGCCTGTGGCCCTCGGAGA 701

Db 125 GCCAGGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGTGCCTGTGGCCCTCGGAGA 184

Qy 702 GCACAGTGTCAAGCAACGGAATCCAGAGCGGAGGTCTACGCCCGCCCTCGGCCACCG 761

Db 185 GCACAGTGTCAAGCAACGGAATCCAGAGCGGAGGTCTACGCCCGCCCTCGGCCACCG 244

Qy 762 ACGGCTTGGCGTGGCGCCCTTTCAGCGGAGCGCTTTCACCGCTTTCAGCGGAGCG 821

Db 245 ACGGCTTGGCGTGGCGCCCTTTCAGCGGAGCGCTTTCACCGCTTTCAGCGGAGCG 304

Qy 822 ATCCGTACCTGAGCAGCAGATCGCTGCCACCCACCATCTCGCTGTGAGCGGGAGG 881

Db 305 ATCCGTACCTGAGCAGCAGATCGCTGCCACCCACCATCTCGCTGTGAGCGGGAGG 364

Qy 882 AGCCCCACCTTACAGGGCCCTTGCACCTTCCAGTTCGGGACCCCGAGCAGCAGCTGG 941

Db 365 AGCCCCACCTTACAGGGCCCTTGCACCTTCCAGTTCGGGACCCCGAGCAGCAGCTGG 424

Qy 942 AACTGAAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACAGTACCTGA 1001

Db 425 AACTGAAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCGACAGTACCTGA 484

Qy 1002 TGGATAGTCCAGGCTGGCGGCCCTTGCACCTTCCAGTTCGGGACCCCGAGCAGCAG 1061

Db 485 TGGATAGTCCAGGCTGGCGGCCCTTGCACCTTCCAGTTCGGGACCCCGAGCAGCAG 544

Qy 1062 CBTGTACCGGAGCGCGGCGCATGAGGGGCGCGCCACCTTACAGCAGGTCATCG 1121

Db 545 CBTGTACCGGAGCGCGGCGCATGAGGGGCGCGCCACCTTACAGCAGGTCATCG 604

Qy 1122 GCACTACCGGGGTCTCTTCCAGCAGCAGGAGTGGGGCGCGCCCTTCTTGTCTGG 1181

Db 605 GCACTACCGGGGTCTCTTCCAGCAGCAGGAGTGGGGCGCGCCCTTCTTGTCTGG 664

Qy 1182 AGGGAGCCCGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 1241

Db 665 AGGGAGCCCGGCTCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 724

Qy 1242 AAGAGAAGGATTAACAGAAAGGACACCTTCTTAG 1276

Db 725 AAGAGAAGGATTAACAGAAAGGACACCTTCTTAG 759

Search completed: February 19, 2005, 22:03:56

Job time : 5702.7 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 16:16:01 ; Search time 707.116 Seconds
(without alignments)
11058.969 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcgagcgca.....ctgcgtagtgaaagagcg 1321

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 4390206 seqs, 2959870667 residues

Word size : 0

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : N_Geneseq_16Dec04:*
1: Geneseqn1980s:*
2: Geneseqn1990s:*
3: Geneseqn2000s:*
4: Geneseqn2001as:*
5: Geneseqn2001bs:*
6: Geneseqn2002as:*
7: Geneseqn2002bs:*
8: Geneseqn2003as:*
9: Geneseqn2003bs:*
10: Geneseqn2003cs:*
11: Geneseqn2003ds:*
12: Geneseqn2004as:*
13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	6	ABK12137 Human cDN
2	1301	98.5	4911	13	ACN40804
3	1229	93.0	4839	8	ACC49552 Tumour-as
4	1229	93.0	4839	11	ADP65809 Human STA
5	1229	93.0	4839	11	ADP65729 Human tra
6	1229	93.0	4839	12	ADM67045 Human hom
7	1229	93.0	4839	13	ADR65875 Human pro
8	1229	93.0	4839	13	ADR66778 Human pro
9	1178	89.2	1383	10	ADC37326 Nuclear f
10	864	65.4	864	11	ADN38809 Cancer/an
11	800	60.6	1140	6	ABK92120 Prostate
12	800	60.6	1140	10	AAD60105 Human and
13	800	60.6	1140	10	ADH62276 Human PME
14	800	60.6	1140	12	ADO39826 Human PME
15	800	60.6	1141	10	ADB75588 Prostate
16	800	60.6	1850	8	ACC49536 Tumour-as
17	800	60.6	4527	11	ADL83313 Human and
18	788	59.7	1066	4	AAI57868 Human pol
19	755	57.2	759	10	ADF17545 Human and
20	755	57.2	759	10	ADH62277 Human PME

21	755	57.2	759	12	ADO39827	Ado39827 Human PME
22	749	56.7	969	3	AAA75151	Aaa75151 cDNA enco
23	749	56.7	1061	3	AAA47429	Aaa47429 Sequence
24	749	56.7	1085	10	ADC37324	Abz37324 Nuclear f
25	749	56.7	1334	8	ABZ36103	Abz36103 Human sec
26	744	56.3	969	3	AAA75163	Abz75163 cDNA clon
27	713	54.0	806	8	ACC49537	Acc49537 Tumour-as
28	698	52.8	969	3	AAA75164	Aaa75164 cDNA clon
29	698	52.8	969	3	AAA75165	Aaa75165 cDNA clon
30	560	42.4	1583	6	ABS61424	Abs61424 Prostate
C 31	409	31.0	711	12	ADO00336	Ado00336 Novel hum
C 32	409	31.0	711	12	ADN98767	Adn98767 Novel hum
C 33	401	30.4	408	5	AAF65983	Aaf65983 Novel hum
C 34	394	29.8	1089	4	AAI59654	Aai59654 Human pol
C 35	364	27.6	474	10	ABZ84732	Abz84732 Toxicolog
C 36	302	22.9	693	6	ABK12143	Abk12143 Human MIV
C 37	271	20.5	812	2	AZS2964	Aaz52964 Human pro
C 38	229	17.3	254	3	AAA41265	Aaa41265 Human sec
C 39	178	13.5	467	9	ACH14862	Ach14862 Human adu
C 40	106	8.0	1879	5	AAS84503	Aas84503 DNA encod
C 41	63	4.8	426	5	AAS84502	Aas84502 DNA encod
C 42	60	4.5	60	6	ABN40872	Abn40872 Human spl
C 43	56	4.2	522	6	ABT10027	Abt10027 Human bre
C 44	51	3.9	51	4	AAH89714	Aah89714 Human cod
C 45	45	3.4	837	6	ABQ43501	Abq43501 Oligonucl

ALIGNMENTS

RESULT 1	ABK12137	standard; cDNA; 1321 BP.
XX	ABK12137;	
XX	05-JUN-2002	(first entry)
XX	Human cDNA encoding Mechanically Induced Vascular Receptor 1, MIVR-1.	
XX	Human; ss; gene; MIVR-1; Mechanically Induced Vascular Receptor 1;	
XX	Cytostatic; cardiant; cerebroprotective; antiarteriosclerotic;	
XX	cardiac cell; anti-apoptotic; vascular endothelial cell;	
XX	cardiac hypertrophy; myocardial infarction; stroke; arteriosclerosis;	
XX	heart failure.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	413..1276
XX	FT	/*tag= a
XX	FT	/product= "MIVR-1"
XX	FT	/note= "This region is specifically claimed in claim 3"
XX	WO200216416-A2.	
XX	28-FEB-2002.	
XX	21-AUG-2001; 2001WO-US026089.	
XX	22-AUG-2000; 2000US-0227159P.	
XX	(BGMH) BRIGHAM & WOMENS HOSPITAL INC.	
XX	(PFIZ) PFIZER INC.	
XX	Lee RT, Landschulz KT, Kennedy SP, Thompson JF, Turi TG;	
XX	WPI; 2002-280912/32.	
XX	P-PSDB; AAU78231.	
XX	Novel nucleic acid molecule encoding Mechanically Induced Vascular	
XX	Receptor-1 polypeptide, useful for treating cardiovascular diseases.	

PS Claim 2; Page 87-88; 105pp; English.

XX The invention relates to an isolated nucleic acid molecule encoding a

CC Mechanically Induced Vascular Receptor (MIVR)-1 polypeptide having

CC cardiac cell anti-apoptotic activity and fragments of it provided they

CC are not identical to Genbank sequences A176141.1, A1594390, NM_004338

CC and A0177461. Also included are expression vectors, host cells, the MIVR-

CC 1 polypeptide, MIVR-1 binding peptides, modulators of MIVR-1, contacting

CC a molecule having cardiac cell anti-apoptotic activity with a candidate

CC agent, where the molecule is a nucleic acid molecule comprising MIVR-1,

CC IEX-1, VDUP-1, BTG-2 and TIS-11d or its expression product, determining

CC if the anti-apoptotic activity is modulated and thereby identifying a

CC modulator. The cardiac cell anti-apoptotic molecules and nucleic acids

CC of the invention are useful for treating, diagnosing and monitoring

CC progression of such diseases and disorders as characterised by increased

CC apoptotic cell-death of vascular endothelial cells e.g. cardiac

CC hypertrophy, myocardial infarction, stroke, arteriosclerosis and heart

CC failure. The present sequence encodes human MIVR-1

XX

SQ Sequence 1321 BP; 223 A; 493 C; 440 G; 165 T; 0 U; 0 Other;

Query Match 100.0%; Score 1321; DB 6; Length 1321;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGCGGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGG 60

DB 1 CGACCGCGGTCTCGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGCGG 60

QY 61 CGCGCGCGCGCGCGCGCGCGCTGCTGGTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120

DB 61 CGCGCGCGCGCGCGCGCGCGCTGCTGGTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120

QY 121 GCGCGAGCGCGCGCGCGCGCTGCGAGCCATTTTCGAGCGCCACCGCGGCGACTGCCG 180

DB 121 GCGCGAGCGCGCGCGCGCGCTGCGAGCCATTTTCGAGCGCCACCGCGGCGACTGCCG 180

QY 181 ACGCCCG 240

DB 181 ACGCCCG 240

QY 241 TGAGCG 300

DB 241 TGAGCG 300

QY 301 CTCCCG 360

DB 301 CTCCCG 360

QY 361 CCCCG 420

DB 361 CCCCG 420

QY 421 CTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

DB 421 CTTGATGGGGGTCAACAGCACCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 480

QY 481 GTGCACTGCAACCGCTCTTTGTTTCAGAGCATGGAGATCAACGAGCTGGAGTTGTTC 540

DB 481 GTGCACTGCAACCGCTCTTTGTTTCAGAGCATGGAGATCAACGAGCTGGAGTTGTTC 540

QY 541 GATCATCATCATCGTGGTGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600

DB 541 GATCATCATCATCGTGGTGTGATGATGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 600

QY 601 CCACTCAAGCTGTCTGACAGCTCTTTCATCAGCGCGCACAGCGGCGGAGGAGAGA 660

DB 601 CCACTCAAGCTGTCTGACAGCTCTTTCATCAGCGCGCACAGCGGCGGAGGAGAGA 660

QY 661 AGATGCCCTGTCTCAGAGGATGCCCTGTGGCGCTTGGAGAGCACAGTGTTCAGGCAACGG 720

DB 661 AGATGCCCTGTCTCAGAGGATGCCCTGTGGCGCTTGGAGAGCACAGTGTTCAGGCAACGG 720

QY 721 AATCCAGAGCGCGAGGTGTACGCCCGCGCTGCGGCCACCGACCGCTGCGCGTGC CGCC 780

DB 721 AATCCAGAGCGCGAGGTGTACGCCCGCGCTGCGGCCACCGACCGCTGCGCGTGC CGCC 780

QY 781 CTTCCGCCAGCGGAGCGGTTCACCGCTTCAGGCCACCTATCCGTACCTGCGAGCACGA 840

DB 781 CTTCCGCCAGCGGAGCGGTTCACCGCTTCAGGCCACCTATCCGTACCTGCGAGCACGA 840

QY 841 GATCGACCTGCGACCCACCATCTCGTGTTCAGACGGGAGGAGCCGCCCTTACCGAGG 900

DB 841 GATCGACCTGCGACCCACCATCTCGTGTTCAGACGGGAGGAGCCGCCCTTACCGAGG 900

QY 901 CCGCTGCACTTCAGCTTCGGGACCCCGAGCAGCTGGAAGTGAACCGGGAGTCCGT 960

DB 901 CCGCTGCACTTCAGCTTCGGGACCCCGAGCAGCTGGAAGTGAACCGGGAGTCCGT 960

QY 961 GCGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTGATGATAGTGCAGGCTGGG 1020

DB 961 GCGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTGATGATAGTGCAGGCTGGG 1020

QY 1021 CGGCCCTGCGCCCGCGAGTAATTCGGGCGATCAGCGCCACGTGTACGGCAGCGCGCG 1080

DB 1021 CGGCCCTGCGCCCGCGAGTAATTCGGGCGATCAGCGCCACGTGTACGGCAGCGCGCG 1080

QY 1081 GCGCATGAGGCG 1140

DB 1081 GCGCATGAGGCG 1140

QY 1141 CTTCCAGCACGAGCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200

DB 1141 CTTCCAGCACGAGCAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1200

QY 1201 CACACATCG 1260

DB 1201 CACACATCG 1260

QY 1261 AGACACCTCTCTAGGCTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320

DB 1261 AGACACCTCTCTAGGCTCCCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1320

QY 1321 G 1321

DB 1321 G 1321

RESULT 2

ACN40804

ID ACN40804 standard; cDNA; 4911 BP.

XX ACN40804;

AC AC

XX AC

XX AC

DT 18-NOV-2004 (first entry)

XX

DE Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.

XX

KW Tumour-associated antigenic target; TAT; human; overexpression; cancer;

KW tumour; diagnosis; cell proliferative disorder; breast cancer;

KW colorectal cancer; lung cancer; ovarian cancer; liver cancer;

KW central nervous system cancer; bladder cancer; pancreatic cancer;

KW cervical cancer; melanoma; leukaemia; hybridisation probe;

KW chromosome identification; chromosome mapping; gene mapping;

XX gene therapy; cytostatic; gene; ss.

XX

OS Homo sapiens.

XX

XX WO2004030615-A2.

PN

XX

XX 15-APR-2004.

PD

XX

XX 29-SEP-2003; 2003WO-US028547.

PF

XX

XX 02-OCT-2002; 2002US-0414971P.

PR

XX

QY 1233 TCTGGAGCAAGAGAGTAACAGAAAGAGACACCTCTCTAGGCTCCCGGGGGCC 1292
DB 1141 TCTGGAGCAAGAGAGTAACAGAAAGAGACACCTCTCTAGGCTCCCGGGGGCC 1200
QY 1293 GGGCTGGGGCTGGCTAGGTGAAAGGCGAG 1321
DB 1201 GGGCTGGGGCTGGCTAGGTGAAAGGCGAG 1229

RESULT 6

ADM67045
ID ADM67045 standard; DNA; 4839 BP.
AC ADM67045;
XX
XX
DT 03-JUN-2004 (first entry)
XX
DE Human homologue of murine adipocyte specific DNA SeqID 180.
XX
XX human; adipocyte specific; ds; adipose tissue; anti-obesity;
KW high mobility group I-C protein; HMGI-C; obesity; leptin; ob; diabetes;
KW adipogenesis; hypertension; cardiovascular disease; anorectic;
KW antidiabetic; hypotensive.
XX
OS Homo sapiens.
XX
XX WO2004011618-A2.
XX
PD 05-FEB-2004.
XX
PF 29-JUL-2003; 2003WO-US023684.
XX
PR 29-JUL-2002; 2002US-0398785P.
PR 12-JUN-2003; 2003US-0478206P.
XX
XX (HMGE-) HMGENCE INC.
XX
XX Chada K, Chouinard R, Ashar H, Sayed AMD;
PI WPI; 2004-143846/14.
XX
XX Identifying adipocyte specific genes, useful for treating obesity or
PT diabetes, and for identifying drug targets, by differential gene
PT expression analysis between adipose tissue or stromal vascular tissue of
PT mice of different genotypes.
XX
PS Claim 11; SEQ ID NO 180; 91pp; English.
XX
CC This invention relates to a novel method for identifying genes that are
CC over-expressed in adipose tissue and as such it provides targets for anti
CC -obesity pharmaceutical compositions. Specifically, it refers to a high
CC mobility group I-C protein (HMGI-C) that is associated with obesity and
CC is epistatic to leptin, furthermore, it refers to the ob gene where an
CC autosomal recessive trait is linked to obesity and diabetes. The present
CC invention describes performing differential gene expression analysis
CC between the white adipose tissue (WAT) or stromal vascular tissue (SVT)
CC of any two different mice selected from a group consisting of wild-type,
CC HMGI-C -/-, ob/ob, or HMGI-C +/- ob/ob genotype mice. Accordingly, using
CC this method novel nucleotides and the encoded proteins thereof were
CC identified that are adipocyte specific, and as such can be used for
CC preventing adipogenesis, diagnosing and treating diabetes, obesity,
CC hypertension and cardiovascular disease, as well as screening for
CC compounds that can modulate or prevent adipogenesis and treat diabetes or
CC obesity. These compositions exhibit anorectic, antidiabetic and
CC hypotensive activities. This polynucleotide sequence is a human homologue
CC of a murine adipocyte specific DNA sequence of the invention.
XX
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.08; Score 1229; DB 12; Length 4839;
Best Local Similarity 100.0%; Pred. NO. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGCGAGCGCGCCCGCTCCGACGCCATT 152
DB 1 GGAAGCTAGCGGACAGAGGCTCAGCCCGCGGCGAGCGCGCCCGCTCCGACGCCATT 60
QY 153 TTCCGACGCGCACCCCGCGGCGACTGCGCGAGCCCGCGGCGCTCCGAGGGGAGGCGCGGG 212
DB 61 TTCCGAGCGCCACCCCGCGGCGACTGCGCGAGCCCGCGGCGCTCCGAGGGGAGGCGCGGG 120
QY 213 GGGCGAGCGGAGCGCGGCTCCCGCGCACTGAGCGCCCGCGGCGCCCGCGGAACTTGGCGGC 272
DB 121 GGGCGAGCGGAGCGCGGCTCCCGCGCACTGAGCGCCCGCGGCGCCCGGAACTTGGCGGC 180
QY 273 GACCCGAGCCCGCGGAGCGGCGCGCTCCCGCGCGCGCGCGCTCTCTCATGCGGGGC 332
DB 181 GACCCGAGCCCGCGGAGCGGCGCGCTCCCGCGCGCGCGCTCTCTCATGCGGGGC 240
QY 333 CCAGAGCTCCGGGCGCGGCGGAGCGCCCGCGGCGCGCCCGCGGCGCCCGCGC 392
DB 241 CCAGAGCTCCGGGCGCGGCGGAGCGCCCGCGGCGCGCCCGCGGCGCCCGCGC 300
QY 393 GCCGCGCGCGCGCGCGCTCATGCAACCGTTGATGGGGTCAACAGACACCGCGCGCGCG 452
DB 301 GCCGCGCGCGCGCGCGCTCATGCAACCGTTGATGGGGTCAACAGACACCGCGCGCGCG 360
QY 453 CGCGCGGCGAGCGCCCAATGCTCTCTGCACTGCACTGCACTGCACTGCTTTTTCAGAGCA 512
DB 361 CGCGCGGCGAGCGCCCAATGCTCTCTGCACTGCACTGCACTGCTTTTTCAGAGCA 420
QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCATCATCATCATCATCATCATCAT 572
DB 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCATCATCATCATCATCATCATCAT 480
QY 573 TGGTGGTGGTATCAGCTGCTCTGAGCCACTACAAGTGTCTGCAAGTCTCTTCATCA 632
DB 481 TGGTGGTGGTATCAGCTGCTCTGAGCCACTACAAGTGTCTGCAAGTCTCTTCATCA 540
QY 633 GCCGCGACAGCGGCGGAGAGAGATGCTCTCTCAGAGAGATGCTCTGAGG 692
DB 541 GCCGCGACAGCGGCGGAGAGAGATGCTCTCTCAGAGAGATGCTCTGAGG 600
QY 693 CTTGCGAGAGCAGGTGTCAGGCAACGGAATCCAGAGCGCGAGTCTACGCCCGGCTC 752
DB 601 CTTGCGAGAGCAGGTGTCAGGCAACGGAATCCAGAGCGCGAGTCTACGCCCGGCTC 660
QY 753 GGGCCACCGACCGCTGGCGCTGCGCGCTTCCGCCAGCGGAGCGGTTCACCGCTTC 812
DB 661 GGGCCACCGACCGCTGGCGCTGCGCGCTTCCGCCAGCGGAGCGGTTCACCGCTTC 720
QY 813 AGCCCACTATTCGTATCTGAGCAGAGATGCACTGCACTGCACTGCACTGCTGTGTCAG 872
DB 721 AGCCCACTATTCGTATCTGAGCAGAGATGCACTGCACTGCACTGCTGTGTCAG 780
QY 873 ACGGGAGGAGCGCCCGACCTTACAGGCGCCCTGCACTGCACTGCACTGCGGAGCCCGGAGC 932
DB 781 ACGGGAGGAGCGCCCGACCTTACAGGCGCCCTGCACTGCACTGCACTGCGGAGCCCGGAGC 840
QY 933 AGCAGCTGGAACCTGAACCGGGAGTCTGGTGGCGCGCACCCCGCAAGAACCATCTTCGACA 992
DB 841 AGCAGCTGGAACCTGAACCGGGAGTCTGGTGGCGCGCACCCCGCAAGAACCATCTTCGACA 900
QY 993 GTGACTGTGATGATGTCAGGCTGGGCGGCGCTGCGCGCCCGCGAGCAGTAACTCGGGCA 1052
DB 901 GTGACTGTGATGATGTCAGGCTGGGCGGCGCTGCGCGCCCGCGAGCAGTAACTCGGGCA 960
QY 1053 TCAGCGCCAGCTGCTACGCGAGCGGCGGCGATGAGGGGCGCGCGCCCGCGCTACAGCG 1112
DB 961 TCAGCGCCAGCTGCTACGCGAGCGGCGGCGATGAGGGGCGCGCGCGCGCGCTACAGCG 1020
QY 1113 AGGTCTATCGGCACTACCGGGGTCTCTCTTCAGCAGCAGCAGAGAGAGTGGGCGCGCT 1172
DB 1021 AGGTCTATCGGCACTACCGGGGTCTCTCTTCAGCAGCAGCAGAGAGAGTGGGCGCGCT 1080

QY 1173 CCTTGTGGAGGGAGCCCGCTCCACACACACATCGCGGCCCTAGAGAGCGGACGCA 1232
Db 1081 CCTTGTGGAGGGAGCCCGCTCCACACACACATCGCGGCCCTAGAGAGCGGACGCA 1140
QY 1233 TCTGGAGCAAGAGAGGATAAACAAGAGGACACACCTCTCTAGGGTTCCTCCAGGGGGCC 1292
Db 1141 TCTGGAGCAAGAGAGGATAAACAAGAGGACACACCTCTCTAGGGTTCCTCCAGGGGGCC 1200
QY 1293 GGCTGGGGCTGGTGGTGAAGGAGGAG 1321
Db 1201 GGCTGGGGCTGGTGGTGAAGGAGGAG 1229

RESULT 7

ADP65875

ID ADP65875 standard; DNA; 4839 BP.

XX

AC ADP65875;

XX

DT 02-DEC-2004 (first entry)

XX

DE Human prostatic carcinoma derived DNA SEQ ID 71 #1.

XX

XX human; cytostatic; diagnosis; prostatic cancer;

KW differential expression analysis; ds.

XX

XX Homo sapiens.

XX

XX WO2004076614-A2.

PN

XX 10-SEP-2004.

XX

XX 22-FEB-2004; 2004WO-DR000433.

PF

XX 27-FEB-2003; 2003DE-01009985.

PR

XX 14-MAY-2003; 2003DE-01022134.

XX

XX (HINZ/) HINZMANN B.

PA

XX (DAHL/) DAHL E.

PA

XX (ROSE/) ROSENTHAL A.

PA

XX (HERM/) HERMANN K.

PA

XX (PILA/) PILARSKY C.

PA

XX

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;

PI Schmitt A, Beckmann G, Brueemendorf T, Kinnemann H, Roepcke S;

PI

XX Xinzhong L, Staub E;

XX

XX WPI; 2004-653386/63.

DR

XX

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,

PT useful for diagnosis, treatment and in screening for specific binding

PT

XX agents.

XX

XX Claim 1; Page 277; 1607pp; German.

PS

XX

XX This invention describes novel cytostatic polynucleotide and polypeptide

XX sequences which can be used in a method for diagnosing prostatic cancer

CC or the risk of developing prostatic cancer. Diagnosis is based on

CC determining over transcription or over expression of the sequences in

CC prostatic tissue. Screening for inhibitors of the sequences or detection

CC substances involves a binding assay, any compounds that bind are

CC selected, optionally after deconvolution of mixtures. Detection of a

CC predetermined minimum level of the reporter indicates the presence of

CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,

CC short-interfering RNA or ribozymes; an organic molecule of molecular

CC weight below 5000, preferably 300, that binds to the polypeptide; an

CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the

CC polypeptide, preferably humanised or human; an anti-idiotype, non-human

CC (monoclonal) antibody directed against Ab or any of the above derivatised

CC with a reporter group, cell toxin, immunostimulatory molecules and/or

CC radioisotope. The polynucleotides are identified in human prostatic

CC cancer by differential expression analysis, using DNA microarrays,

CC between normal and tumorous tissues, with (over)expression being detected

CC

CC by quantitative PCR. Analysis of prostatic cancer samples showed that

CC CD24 was upregulated in many of them. Sections of tissue, isolated from

CC prostatic cancer patients, or subjects at risk, were incubated

CC sequentially with anti-human CD4 murine monoclonal antibodies;

CC biotinylated second antibody; streptavidin-conjugated horseradish

CC peroxidase and then diaminobenzidine as colour former (brown). The

CC samples were counterstained with hemalum (blue). Malignant cells stained

CC strongly but non-malignant cells only weakly. In 15 of 63 samples of

CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and

CC lymph node metastases were also stained. ADR65805-ADR65954 represent the

CC polynucleotide and polypeptide sequences used in the method of the

CC invention.

XX

SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 13; Length 4839;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGCAGAGGCTCAGCCCCCGCGCGAGCGCGCGCCCGCTGCCAGCCCAT 152

Db 1 GGAAGCTAGCGCAGAGGCTCAGCCCCCGCGCGAGCGCGCGCCCGCTGCCAGCCCAT 60

QY 153 TTCCGGACCCACCGCGGGGCACTGCCGACGCGCGCGCGCGCGCGCGCGCGCGCG 212

Db 61 TTCCGGACCCACCGCGGGGCACTGCCGACGCGCGCGCGCGCGCGCGCGCGCGCG 120

QY 213 GGGCGCAGCGGAGCGGCTCCCGCAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCG 272

Db 121 GGGCGCAGCGGAGCGGCTCCCGCAGCTGAGCGCGCGCGCGCGCGCGCGCGCGCG 180

QY 273 GACCCGAGCG 332

Db 181 GACCCGAGCG 240

QY 333 CCCAGTCTCCGGCG 392

Db 241 CCCAGTCTCCGGCG 300

QY 393 GCG 452

Db 301 GCG 360

QY 453 CCG 512

Db 361 CCG 420

QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGCTGCTGCTGCTGCTGA 572

Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGCTGCTGCTGCTGA 480

QY 573 TGA 632

Db 481 TGA 540

QY 633 GCGCGCACAGCG 692

Db 541 GCGCGCACAGCG 600

QY 693 CTTGCGAGAGCAGTGTTCAGCAAGCAAGTTCAGAGCGCGCGCGCGCGCGCGCGCGCTC 752

Db 601 CTTGCGAGAGCAGTGTTCAGCAAGCAAGTTCAGAGCGCGCGCGCGCGCGCGCGCTC 660

QY 753 GCGCCACCGCTTC 812

Db 661 GCGCCACCGCTTC 720

QY 813 AGCCACCTATCCGTACCTGCGAGCAGAGATCGAGCTGCCACCCACCATCTCGCTCTCAG 872

Db 721 AGCCACCTATCCGTACCTGCGAGCAGAGATCGAGCTGCCACCCACCATCTCGCTCTCAG 780

QY 873 ACGGGAGAGCG 932

|||||

```
Db 781 ACGGGAGAGCCCCACCTACAGGGCCCTGCACCCCTCCAGCTTCGGGACCCCGAGC 840
Qy 933 AGCAGCTGGAATGAACCGGGAGTGGTGGCGGACCCCCCAACAGAACCATTTGAC 992
Db 841 AGCAGCTGGAATGAACCGGGAGTGGTGGCGGACCCCCCAACAGAACCATTTGAC 900
Qy 993 GTGACCTGATGGATAGTCAGAGCTGGGCGGCGCCCTGCCCGCCAGCAGTAACCTCGGCA 1052
Db 901 GTGACCTGATGGATAGTCAGAGCTGGGCGGCGCCCTGCCCGCCAGCAGTAACCTCGGCA 960
Qy 1053 TCAGCGCAGCTGCTACGCGAGCGGGCGGCGCATGGAGGGCGCGCGCCACCTACAGCG 1112
Db 961 TCAGCGCAGCTGCTACGCGAGCGGGCGGCGCATGGAGGGCGCGCGCCACCTACAGCG 1020
Qy 1113 AGTCTATCGGCCATACCCCGGGTCTCTTCAGCACCAGCAGAGTGGCGCGCCT 1172
Db 1021 AGTCTATCGGCCATACCCCGGGTCTCTTCAGCACCAGCAGAGTGGCGCGCCT 1080
Qy 1173 CCTTGTCTGGAGGGACCCGCTCCACACACACATCGCGCCCTAGAGCGCGACCA 1232
Db 1081 CCTTGTCTGGAGGGACCCGCTCCACACACACATCGCGCCCTAGAGCGCGACCA 1140
Qy 1233 TCTGGAGCAAGAGAGGATAAACAAGAGGACACCTCTCTAGGGTCCCGAGGGGGCC 1292
Db 1141 TCTGGAGCAAGAGAGGATAAACAAGAGGACACCTCTCTAGGGTCCCGAGGGGGCC 1200
Qy 1293 GGGCTGGGGTCTGCTAGTGAAGGACAG 1321
Db 1201 GGGCTGGGGTCTGCTAGTGAAGGACAG 1229
```

RESULT 8

ADR66778
ID ADR66778 standard; DNA; 4839 BP.

AC ADR66778;

DT 02-DEC-2004 (first entry)

DE Human prostatic carcinoma derived DNA SEQ ID 71 #4.

KW human; cytostatic; diagnosis; prostatic cancer;
KW differential expression analysis; db.

OS Homo sapiens.

XX WO2004076614-A2.

XX 10-SEP-2004.

XX 22-FEB-2004; 2004WO-DR000433.

XX 27-FEB-2003; 2003DE-01009985.

XX 14-MAY-2003; 2003DE-01022134.

XX (HINZ/) HINZMANN B.

XX (DAHL/) DAHL E.

XX (ROSE/) ROSENTHAL A.

XX (HERM/) HERMANN K.

XX (PILA/) PILARSKY C.

XX Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;
PI Schmitt A, Beckmann G, Brueemendorf T, Kinnemann H, Roepcke S;
PI Xinzhang L, Staub E;

XX WPI; 2004-653386/63.

XX New nucleic acids, and encoded proteins, from prostatic cancer tissue,
PT useful for diagnosis, treatment and in screening for specific binding
PT agents.

XX Claim 1; Page 1447; 1607pp; German.

XX

CC This invention describes novel cytostatic polynucleotide and polypeptide
CC sequences which can be used in a method for diagnosing prostatic cancer
CC or the risk of developing prostatic cancer. Diagnosis is based on
CC determining over transcription or over expression of the sequences in
CC prostatic tissue. Screening for inhibitors of the sequences or detection
CC substances involves a binding assay, any compounds that bind are
CC selected, optionally after deconvolution of mixtures. Detection of a
CC predetermined minimum level of the reporter indicates the presence of
CC tumour cells. Inhibitors can be chosen from antisense oligonucleotides,
CC short-interfering RNA or ribozymes; an organic molecule of molecular
CC weight below 5000, preferably 300, that binds to the polypeptide; an
CC aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the
CC polypeptide, preferably humanised or human; an anti-idiotypic, non-human
CC (monoclonal) antibody directed against Ab or any of the above derivatised
CC with a reporter group, cell toxin, immunostimulatory molecules and/or
CC radioisotopes. The polynucleotides are identified in human prostatic
CC cancer by differential expression analysis, using DNA microarrays,
CC between normal and tumorous tissues, with (over)expression being detected
CC by quantitative PCR. Analysis of prostatic cancer samples showed that
CC prostatic cancer patients, or subjects at risk, were incubated
CC sequentially with anti-human CD4 murine monoclonal antibodies;
CC biotinylated second antibody; streptavidin-conjugated horseradish
CC peroxidase and then diaminobenzidine as colour former (brown). The
CC samples were counterstained with hemalum (blue). Malignant cells stained
CC strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC lymph node metastases were also stained. ADR65805-ADR66954 represent the
CC polynucleotide and polypeptide sequences used in the method of the
CC invention.

XX
SQ Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;

Query Match 93.0%; Score 1229; DB 13; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 93 GGAAGCTAGCGGACAGAGCTAGCCCCCGGCGGACGGCGCGCGCGCGCGCCATT 152
Db 1 GGAAGCTAGCGGACAGAGCTAGCCCCCGGCGGACGGCGCGCGCGCGCGCCATT 60
Qy 153 TTCCGGACGCCACCCCGGGGCACTGCGGACGCCCGCGGGGCTGCCGAGGGGCGCGGG 212
Db 61 TTCCGGACGCCACCCCGGGGCACTGCGGACGCCCGCGGGGCTGCCGAGGGGCGCGGG 120
Qy 213 GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCGCGCGCGCGCGCGCGGAACTTGGCGGC 272
Db 121 GGGCGCAGCGGAGCGCGGTCCCGCGCACTGAGCGCGCGCGCGCGCGCGGAACTTGGCGGC 180
Qy 273 GACCCGAGCCCGGCGAGCGGGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGGC 332
Db 181 GACCCGAGCCCGGCGAGCGGGCGCGCTTCCCGCGCGCGCGCGCGCGCGCGCGCGGC 240
Qy 333 CCNAGCTCCGGGCGCGCGCGGAGCCCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 392
Db 241 CCNAGCTCCGGGCGCGCGCGGAGCCCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCG 300
Qy 393 GCGCGCGCGCGCGCGCGCTCATGCACTGATGGGGGTCAACAGCACCGCGCGCGCGCG 452
Db 301 GCGCGCGCGCGCGCGCTCATGCACTGATGGGGGTCAACAGCACCGCGCGCGCGCGCG 360
Qy 453 CGCGCGGCGAGCGCCCAATGTCTCTGCACTGCAACTGCAAAAGCTCTTTGTTCCAGAGCA 512
Db 361 CGCGCGGCGAGCGCCCAATGTCTCTGCACTGCAACTGCAAAAGCTCTTTGTTCCAGAGCA 420
Qy 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTGGTGGTGA 572
Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCTCGTGGTGGTGGTGGTGA 480
Qy 573 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 632
Db 481 TGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 540
```

QY 633 GCCGGCAGCCAGCGGGCGAGGAGAGATGCCCTGTCTCAGAAAGATGCTGTGGC 692
 Db GCCGGCAGCCAGCGGGCGAGGAGAGATGCCCTGTCTCAGAAAGATGCTGTGGC 600
 QY 693 CCTCGGAGACAGTGTTCAGGCAACGGAATCCAGAGCGCAGGTCTAGCCCGCCTC 752
 Db CCTCGGAGACAGTGTTCAGGCAACGGAATCCAGAGCGCAGGTCTAGCCCGCCTC 660
 QY 753 GGCCACCGACCGCTGGCGGTGCGCCCTTCGCCCCAGCGGAGCGCTTCCACGCTTCC 812
 Db GGCCACCGACCGCTGGCGGTGCGCCCTTCGCCCCAGCGGAGCGCTTCCACGCTTCC 720
 QY 813 AGCCACCTATCCGTACTGTCAGCAGCAGATGCACTGCGCACCCACCATCTCGTGTGAG 872
 Db AGCCACCTATCCGTACTGTCAGCAGCAGATGCACTGCGCACCCACCATCTCGTGTGAG 780
 QY 873 ACGGGAGAGCCCGCCACCTTACCAGGGCGCTGCACTTCCAGCTTCGGGACCCCGAGC 932
 Db ACGGGAGAGCCCGCCACCTTACCAGGGCGCTGCACTTCCAGCTTCGGGACCCCGAGC 840
 QY 933 AGCAGCTGGAATGAACCGGAGTGGTGGCGCACCCCGCCAAACAGAACCATCTTCGACA 992
 Db AGCAGCTGGAATGAACCGGAGTGGTGGCGCACCCCGCCAAACAGAACCATCTTCGACA 900
 QY 993 GTGACCTGATGATGATGTCAGAGTGGCGGCGCCCTGCGCCCGCCAGCAGTAATCGGGCA 1052
 Db GTGACCTGATGATGATGTCAGAGTGGCGGCGCCCTGCGCCCGCCAGCAGTAATCGGGCA 960
 QY 1053 TCAGCGCCAGTGTACGCGCAGCGGGCGGCGATGAGGGCGCGCGCCACCTACAGCG 1112
 Db TCAGCGCCAGTGTACGCGCAGCGGGCGGCGATGAGGGCGCGCGCCACCTACAGCG 1020
 QY 1113 AGGTCTATCGGCCACTACCCGGGGTCTCTCTTCAGCACACAGCAGCAGTGGGCGCCCT 1172
 Db AGGTCTATCGGCCACTACCCGGGGTCTCTCTTCAGCACACAGCAGCAGTGGGCGCCCT 1080
 QY 1173 CTTGTGTGAGGGGACCCCGCTCCACACACATGCGCGCCCTTAGAGAGCGCAGCCA 1232
 Db CTTGTGTGAGGGGACCCCGCTCCACACACATGCGCGCCCTTAGAGAGCGCAGCCA 1140
 QY 1233 TCTGGAGCAAGAGAGGATACAGAAAGGACACCTCTCTTAGGCTCCCGAGGGGGCC 1292
 Db TCTGGAGCAAGAGAGGATACAGAAAGGACACCTCTCTTAGGCTCCCGAGGGGGCC 1200
 QY 1293 GGGCTGGGGCTGGGTAGTGAAGAGCAG 1321
 Db GGGCTGGGGCTGGGTAGTGAAGAGCAG 1229

RESULT 9

ADC37326
 ID ADC37326 standard; DNA; 1383 BP.
 XX
 AC ADC37326;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE Nuclear factor kappa B (NF-kappaB) activating gene, SEQ ID 159.
 XX
 KW Nuclear factor kappa B; NF-kappaB; inflammation; autoimmune disease;
 KW cancer; infectious disease; bone disease; AIDS;
 KW neurodegenerative disease; ischemic disorder; Antinflammatory;
 KW Immunomodulator; Cytostatic; Antimicrobial; Osteopathic; Anti-Hiv;
 KW Neuroprotective; Nootropic; Cardiant; Gene therapy; human; gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO2003048202-A2.
 XX
 PD 12-JUN-2003.
 XX
 PF 03-DEC-2002; 2002WO-JP012644.
 XX

PR 03-DEC-2001; 2001JP-00368692.
 PR 05-DEC-2001; 2001US-0335829P.
 PR 03-OCT-2002; 2002JP-00291302.
 PR 04-OCT-2002; 2002US-0415769P.

XX (ASAH) ASAH KASEI KK.

XX Matsuda A, Muramatsu S;

XX WPI; 2003-505282/47.

DR P-PSDB; ADC37327.

XX
 PT New purified protein that activates nuclear factor kappa B (NF-kappaB),
 PT useful for treating inflammation, autoimmune diseases, cancers,
 PT infectious diseases, bone diseases, AIDS, neurodegenerative diseases or
 PT ischemic disorders.

XX Claim 4; SEQ ID NO 159; 938pp; English.

XX The present invention relates to novel proteins and their coding
 CC sequences (ADC37168-ADC37455), which activate nuclear factor kappa B (NF-
 CC kappaB). The proteins and their coding sequences are useful for treating
 CC a disease associated with NF-kappaB activation, such as inflammation,
 CC autoimmune diseases, cancers, infectious diseases, bone diseases, AIDS,
 CC neurodegenerative diseases, or ischemic disorders.

XX Sequence 1383 BP; 253 A; 505 C; 440 G; 185 T; 0 U; 0 Other;

Query Match 89.2%; Score 1178; DB 10; Length 1383;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 1228; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 93 GGAAGCTAGCGCAGAGGCTCAGCCCGCGCGCAGCGCGCGCTGCCAGGCCATT 152
 Db 1 GGAAGCTAGCGCAGAGGCTCAGCCCGCGCGCAGCGCGCGCTGCCAGGCCATT 60

QY 153 TTCCGAGACCCACCGCGCGCCTGCGGAGCGCGCGCGCGCGCGCGCGCGCGCG 212

Db 61 TTCCGAGACCCACCGCGCGCCTGCGGAGCGCGCGCGCGCGCGCGCGCGCG 120

QY 213 GGGCGCAGCGAGCGGGTCCCGGACATGAGCCCGCGCGCGCGCGCGCGCGCG 272

Db 121 GGGCGCAGCGAGCGGGTCCCGGACATGAGCCCGCGCGCGCGCGCGCGCGCG 180

QY 273 GACCCGAGCG 332

Db 181 GACCCGAGCG 240

QY 333 CCCAGCTCGGCG 392

Db 241 CCCAGCTCGGCG 300

QY 393 GCGGCG 452

Db 301 GCGGCG 360

QY 453 CG 512

Db 361 CG 420

QY 513 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGTGATGATG 572

Db 421 TGGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGTGATGATG 480

QY 573 TGGTGGTGGTATCAGTGCCTGTCAGCAGCTACAGCTGTCTGACGGTCTTCATCA 632

Db 481 TGGTGGTGGTATCAGTGCCTGTCAGCAGCTACAGCTGTCTGACGGTCTTCATCA 540

QY 633 GCCCGCACAGCGGGCGGAGGAGAGATGCCCTGTCTCAGAAAGATGCCCTGTGCG 692

Db 541 GCCCGCACAGCGGGCGGAGGAGAGATGCCCTGTCTCAGAAAGATGCCCTGTGCG 600

QY 693 CCTCGGAGACAGTGTTCAGGCAACCGGAATCCAGAGCGCGCGCGCGCGCTC 752

Best Local Similarity 100.0%; Pred. No. 3e-05;
Matches 34; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCGCG 78
|||||
Db 226 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 193

RESULT 4

US-09-640-211A-1198/c
; Sequence 1198, Application US/09640211A

; Patent No. 6833446

; GENERAL INFORMATION:

; APPLICANT: Wood, Marion

; APPLICANT: Shenk, Michael A.

; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions and Methods for the
Modification of Gene Transcription

; FILE REFERENCE: 11000.1021CIU

; CURRENT FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 2368

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1198

; LENGTH: 359

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

US-09-640-211A-1198

Query Match 2.3%; Score 31; DB 4; Length 359;

Best Local Similarity 100.0%; Pred. No. 0.00065;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
|||||

Db 206 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 176
|||||

RESULT 5

US-09-640-211A-1340/c

; Sequence 1340, Application US/09640211A

; Patent No. 6833446

; GENERAL INFORMATION:

; APPLICANT: Wood, Marion

; APPLICANT: Shenk, Michael A.

; APPLICANT: McGrath, Annette

; APPLICANT: Glenn, Matthew

; TITLE OF INVENTION: Compositions and Methods for the
Modification of Gene Transcription

; FILE REFERENCE: 11000.1021CIU

; CURRENT FILING DATE: 2000-08-16

; NUMBER OF SEQ ID NOS: 2368

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1340

; LENGTH: 533

; TYPE: DNA

; ORGANISM: Eucalyptus grandis

US-09-640-211A-1340

Query Match 2.3%; Score 31; DB 4; Length 533;

Best Local Similarity 100.0%; Pred. No. 0.00064;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 75
|||||

Db 97 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 67
|||||

RESULT 6

US-09-949-016-13247

; Sequence 13247, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 13247

; LENGTH: 11729

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-13247

Query Match 2.3%; Score 30; DB 4; Length 11729;

Best Local Similarity 100.0%; Pred. No. 0.0014;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 GAGGAGGAGGAGCGCGCGCGCGCGCGCGCG 74
|||||

Db 10019 GAGGAGGAGGAGCGCGCGCGCGCGCGCG 10048
|||||

RESULT 7

US-09-949-016-15127

; Sequence 15127, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCE: CL001307

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 15127

; LENGTH: 142783

; TYPE: DNA

; ORGANISM: Human

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(142783)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-15127

Query Match 2.3%; Score 30; DB 4; Length 142783;

Best Local Similarity 100.0%; Pred. No. 0.0011;

Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 554 GTGGTGTGATGATGATGATGATGATGATG 583
|||||

Db 23669 GTGGTGTGATGATGATGATGATGATG 23698
|||||

RESULT 8

US-09-949-016-1263/c

; Sequence 1263, Application US/09949016

; Patent No. 6812339

RESULT 12
US-09-949-016-13765/c
; Sequence 13765, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949, 016

;; CURRENT FILING DATE: 2000-04-14
;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13765
;; LENGTH: 128470
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-13765

Query Match 2.2%; Score 29; DB 4; Length 128470;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 555 TGGTGTGATGATGATGATGATGATGATG 583
Db 98598 TGGTGTGATGATGATGATGATGATG 98570

RESULT 13
US-09-236-097-7
; Sequence 7, Application US/09236097
; Patent No. 6335165
; GENERAL INFORMATION:
; APPLICANT: NIR NAVOT ET AL
; TITLE OF INVENTION: METHODS AND KITS FOR CHARACTERIZING GC
; TITLE OF INVENTION: -RICH NUCLEIC ACID SEQUENCES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
; STREET: 20001 Jefferson Davis Highway, Suite 207
; CITY: Arlington
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
; COMPUTER: Twinhead* Slimnote-890TX
; OPERATING SYSTEM: MS DOS version 6.2,
; OPERATING SYSTEM: Windows version 3.11
; SOFTWARE: Word for Windows version 2.0 converted to
; SOFTWARE: an ASCII file
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/236,097
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; APPLICANT INFORMATION:
; NAME: Friedman, Mark M.
; REGISTRATION NUMBER: 33,883
; REFERENCE/DOCKET NUMBER: 128/33
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 972-3-562553
; TELEFAX: 972-3-562554
; TELEX:
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 700
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-236-097-7

Query Match 2.1%; Score 28; DB 3; Length 700;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGGCGGCG 83
Db 505 GGCGGCGGCGGCGGCGGCGGCGGCGGCG 532

RESULT 14
US-09-086-010-1
; Sequence 1, Application US/09086010
; Patent No. 6274338
; GENERAL INFORMATION:
; APPLICANT: Glimcher, Laurie H. et al.
; TITLE OF INVENTION: Human c-Maf Compositions and
; TITLE OF INVENTION: Methods of Use Thereof
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,010
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/030,579
; FILING DATE: 2-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Kara, Catherine J.
; REGISTRATION NUMBER: 41,106
; REFERENCE/DOCKET NUMBER: HUI-027CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-4214
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1203 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1203
US-09-086-010-1

Query Match 2.1%; Score 28; DB 3; Length 1203;
Best Local Similarity 100.0%; Pred. No. 0.013;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 56 GGCGGCGGCGGCGGCGGCGGCGGCGGCG 83
Db 679 GGCGGCGGCGGCGGCGGCGGCGGCGGCG 706

RESULT 15
US-07-705-490-1
; Sequence 1, Application US/07705490
; Patent No. 6107025
; GENERAL INFORMATION:
; APPLICANT: Caskey, C. T.
; APPLICANT: Nelson, David L.
; APPLICANT: Pieretti, Maura
; APPLICANT: Warren, Stephen T.
; APPLICANT: Oostria, Ben A.
; TITLE OF INVENTION: Diagnosis of the Fragile X Syndrome

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
OM nucleic - nucleic search, using sw model
Run on: February 19, 2005, 19:27:04 ; Search time 742.23 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgggtctcgagcgca.....ctgcgtaggtgaaagcgag 1321

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 5384158 seqs, 2955248155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

- Database : Published Applications NA:*
- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
 - 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
 - 3: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
 - 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
 - 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
 - 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
 - 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
 - 9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
 - 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
 - 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
 - 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
 - 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
 - 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
 - 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
 - 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
 - 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
 - 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
 - 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
 - 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
 - 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
 - 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1321	100.0	1321	9	US-09-934-249-1
2	1229	93.0	4839	15	US-10-241-220-119
3	1229	93.0	4839	16	US-10-269-909-84
4	1229	93.0	4839	16	US-10-269-909-85
5	1229	93.0	4839	18	US-10-872-972-119
6	1229	93.0	4839	18	US-10-872-991-119
7	864	65.4	864	17	US-10-295-027-127
8	861	65.2	861	9	US-09-934-249-3
9	800	60.6	1140	16	US-10-390-045-1
10	800	60.6	1140	17	US-10-434-479-1
11	800	60.6	1141	15	US-10-205-823-412

12	800	60.6	1141	15	US-10-301-822-208	Sequence 208, Appl	
13	800	60.6	1850	15	US-10-241-220-44	Sequence 44, Appl	
14	800	60.6	1850	18	US-10-872-972-44	Sequence 44, Appl	
15	800	60.6	1850	18	US-10-872-991-44	Sequence 44, Appl	
16	800	60.6	4527	10	US-09-821-813-2	Sequence 2, Appl1	
17	800	60.6	4527	18	US-10-849-635-2	Sequence 2, Appl1	
18	788	59.7	1066	13	US-10-098-841-71	Sequence 71, Appl	
19	755	57.2	759	16	US-10-390-045-2	Sequence 2, Appl1	
20	755	57.2	759	17	US-10-434-479-2	Sequence 2, Appl1	
21	749	56.7	969	10	US-09-796-753-55	Sequence 55, Appl	
22	713	54.0	806	15	US-10-241-220-45	Sequence 45, Appl	
23	713	54.0	806	18	US-10-872-972-45	Sequence 45, Appl	
24	713	54.0	806	18	US-10-872-991-45	Sequence 45, Appl	
25	560	42.4	1583	14	US-10-000-256A-32	Sequence 32, Appl	
c	26	302	22.9	693	9	US-09-934-249-14	Sequence 14, Appl
27	178	13.5	467	10	US-09-918-995-2074	Sequence 2074, Ap	
28	102	7.7	368	9	US-09-783-590-3464	Sequence 3464, Ap	
29	60	4.5	60	10	US-09-908-975-13620	Sequence 13620, A	
30	56	4.2	522	17	US-10-240-425-166	Sequence 166, App	
31	50	3.8	65	9	US-09-783-590-3488	Sequence 3488, Ap	
32	45	3.4	837	18	US-10-363-345A-30091	Sequence 30091, A	
c	33	45	3.4	837	18	US-10-363-345A-30092	Sequence 30092, A
34	44	3.3	878	9	US-09-934-249-12	Sequence 12, Appl	
35	44	3.3	1713	10	US-09-796-753-57	Sequence 57, Appl	
36	41	3.1	475	9	US-09-934-249-15	Sequence 15, Appl	
c	37	37	2.8	837	18	US-10-363-345A-30089	Sequence 30089, A
38	37	2.8	837	18	US-10-363-345A-30090	Sequence 30090, A	
39	34	2.6	555	18	US-10-425-115-66221	Sequence 66221, A	
c	40	34	2.6	640	18	US-10-856-499-146	Sequence 146, App
c	41	34	2.6	1050	18	US-10-739-930-3690	Sequence 3690, App
c	42	34	2.6	1752	18	US-10-437-963-48088	Sequence 48088, A
c	43	34	2.6	2000	17	US-10-260-238-2427	Sequence 2427, Ap
44	32	2.4	577	9	US-09-864-761-20542	Sequence 20542, A	
45	32	2.4	630	18	US-10-437-963-45057	Sequence 45057, A	

ALIGNMENTS

RESULT 1

- US-09-934-249-1
- ; Sequence 1, Application US/09934249
 - ; Patent No. US20020115081A1
 - ; GENERAL INFORMATION:
 - ; APPLICANT: Lee, Richard T.
 - ; APPLICANT: Landschulz, Katherine T.
 - ; APPLICANT: Turi, Thomas G.
 - ; APPLICANT: Thompson, John P.
 - ; APPLICANT: Kennedy, Scott P.
 - ; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
 - ; TITLE OF INVENTION: CARDIOVASCULAR CONDITIONS
 - ; FILE REFERENCE: P0738/7001/ERP/KA
 - ; CURRENT APPLICATION NUMBER: US/09/934, 249
 - ; CURRENT FILING DATE: 2001-08-21
 - ; PRIOR APPLICATION NUMBER: US 60/227,159
 - ; PRIOR FILING DATE: 2000-08-22
 - ; NUMBER OF SEQ ID NOS: 17
 - ; SOFTWARE: FastSeq for Windows Version 3.0
 - ; SEQ ID NO 1
 - ; LENGTH: 1321
 - ; TYPE: DNA
 - ; ORGANISM: Homo Sapiens
 - ; FEATURE:
 - ; NAME/KEY: CDS
 - ; LOCATION: (413)...(1273)
- US-09-934-249-1

Query Match 100.0%; Score 1321; DB 9; Length 1321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1321; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGACCGGCTCTCGAGCGCAACCCGATCTCTTGACTTGAATGAGGAGGCGG 60
|||||

Db 1 CGACCGGGTCTCGGAGCGAAACCCGATCTCTTGGACTTGAATGAGGAGGAGGCGG 60
Qy 61 CGGCGGCGGCGGCGGAGCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120
Db 61 CGGCGGCGGCGGCGGAGCGCTCGGCTGGGAAAGCTAGCGGAGAGGCTCAGCCCC 120
Qy 121 GCGGAGAGCGGCGGCGGCTCGGCTCGGAGCGCAATTTTCGGAGCGCAACCCGCGGGGACTGCGG 180
Db 121 GCGGAGAGCGGCGGCGGCTCGGCTCGGAGCGCAATTTTCGGAGCGCAACCCGCGGGGACTGCGG 180
Qy 181 ACGCCCGCGGCTGCGGAGGAGGCGGCGGGGCGCAGCGAGCGCGCTCCCGCGCAC 240
Db 181 ACGCCCGCGGCTGCGGAGGAGGCGGCGGGGCGCAGCGAGCGCGCTCCCGCGCAC 240
Qy 241 TGAGCGCGGCGGCGGCGGCGGAACTTGGCGGCGCAACCGAGCGCGGCGGCGGCGGCGG 300
Db 241 TGAGCGCGGCGGCGGCGGCGGAACTTGGCGGCGCAACCGAGCGCGGCGGCGGCGGCGG 300
Qy 301 CTCCCGCGGCGGCGGCTCTTGATGCGGGGCGGCCAGCTCCGGGCGGCGGCGGAGCGCC 360
Db 301 CTCCCGCGGCGGCGGCTCTTGATGCGGGGCGGCCAGCTCCGGGCGGCGGCGGAGCGCC 360
Qy 361 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Db 361 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 420
Qy 421 CTTGATGGGGGTCAACAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Db 421 CTTGATGGGGGTCAACAGCAGCGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
Qy 481 GTGCACTGCAAAACGCTCTTTGTTCCAGAGCATGGAGATCAGCGAGCTGGAGTTGTTC 540
Db 481 GTGCACTGCAAAACGCTCTTTGTTCCAGAGCATGGAGATCAGCGAGCTGGAGTTGTTC 540
Qy 541 GATCATCATCATGT 600
Db 541 GATCATCATCATGT 600
Qy 601 CCACTACAAGCTGTCTGACGGTCTTTCATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Db 601 CCACTACAAGCTGTCTGACGGTCTTTCATCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 660
Qy 661 AGATGCGCTTCTCAGAAAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 661 AGATGCGCTTCTCAGAAAGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Qy 721 AATCCAGAGCGCGAGGTCTACCGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Db 721 AATCCAGAGCGCGAGGTCTACCGCGGCTTCCGCGGCGGCGGCGGCGGCGGCGGCGGCGG 780
Qy 781 CTTTCGCGCGGAGCGGCTTTCACCGCTTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Db 781 CTTTCGCGCGGAGCGGCTTTCACCGCTTTCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 840
Qy 841 GATGACCTTCCACCAACCATCTCGTGTGTCAGCGGAGGAGCGGCGGCGGCGGCGGCGG 900
Db 841 GATGACCTTCCACCAACCATCTCGTGTGTCAGCGGAGGAGCGGCGGCGGCGGCGGCGG 900
Qy 901 CCGCTGCAACCTTCCAGCTTTCGGAACCGCGAGCAGCAGCTGGAACCTGAAACCGGAGT 960
Db 901 CCGCTGCAACCTTCCAGCTTTCGGAACCGCGAGCAGCAGCTGGAACCTGAAACCGGAGT 960
Qy 961 GCGCGCAACCCCAAAACAGAACCATCTTCGACGTGACCTGATGATGATGATGATGATGAT 1020
Db 961 GCGCGCAACCCCAAAACAGAACCATCTTCGACGTGACCTGATGATGATGATGATGATGAT 1020
Qy 1021 CGGCGCTTGCCTCCCGCAGCAGTAACTCGGCGCATCAGCGCACGTGCTACGGCAGCGCGG 1080
Db 1021 CGGCGCTTGCCTCCCGCAGCAGTAACTCGGCGCATCAGCGCACGTGCTACGGCAGCGCGG 1080
Qy 1081 GCGCATGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140
Db 1081 GCGCATGGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1140

Qy 1141 CTTCCAGCACCAAGCAGAGCAGTGGCGGCGGCTCTTTGCTGGAGGAGACCGGCTCCACCA 1200
Db 1141 CTTCCAGCACCAAGCAGAGCAGTGGCGGCGGCTCTTTGCTGGAGGAGACCGGCTCCACCA 1200
Qy 1201 CACACATGTCGGCGGCTTAGAGAGCGCAGCATCTGGAGCAAGAGATAAACAGAA 1260
Db 1201 CACACATGTCGGCGGCTTAGAGAGCGCAGCATCTGGAGCAAGAGATAAACAGAA 1260
Qy 1261 AGGACACCTCTCTAGGGTCCCAGAGGGGCGGCGGCTGGGCTGCGTAGTGAAGGCA 1320
Db 1261 AGGACACCTCTCTAGGGTCCCAGAGGGGCGGCGGCTGGGCTGCGTAGTGAAGGCA 1320
Qy 1321 G 1321
Db 1321 G 1321

RESULT 2

US-10-241-220-119
; Sequence 119, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-119

Query Match 93.0%; Score 1229; DB 15; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1229; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGAAAGCTAGCGGAGAGCTCAGCCCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCA 152
Db 1 GGAAAGCTAGCGGAGAGCTCAGCCCGGCGGAGCGCGCGCGCGCGCGCGCGCGCGCA 60
Qy 153 TTCGGAGCGCACCGCGGCGGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 212
Db 61 TTCGGAGCGCACCGCGGCGGCTGCGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 120
Qy 213 GCGCGCAGCGGAGCGGCTCCCGCGCAGCTGAGCGCGCGGCGGCGGCGGCGGCGGCGG 272
Db 121 GCGCGCAGCGGAGCGGCTCCCGCGCAGCTGAGCGCGCGGCGGCGGCGGCGGCGG 180
Qy 273 GACCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 332
Db 181 GACCGGAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 240
Qy 333 CCGAGCTCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 392
Db 241 CCGAGCTCCGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
Qy 393 GCGCGCGCGCGCGGCGGCTCCATGACCGCTTGTATGGGGGTCAACAGACCGCGCGCGG 452
Db 301 GCGCGCGCGCGCGGCGGCTCCATGACCGCTTGTATGGGGGTCAACAGACCGCGCGG 360
Qy 453 CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
Db CCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512

[illegible]

QY 882 AGCCCCACCTACAGGGCCCTGACCCCTCCAGCTTCGGGACCCCGAGCAGAGTGG 941
DB 459 AGCCCCACCTACAGGGCCCTGACCCCTCCAGCTTCGGGACCCCGAGCAGAGTGG 518
QY 942 AACTGAACCGGGAGTGGTGGCGGCACCCCAACAGAACCATCTTCGACAGTGACCTGA 1001
DB 519 AACTGAACCGGGAGTGGTGGCGGCACCCCAACAGAACCATCTTCGACAGTGACCTGA 578
QY 1002 TGGATAGTGCAGGGTGGGCGGCGCCCTGCGCCCGCCAGAGTAATCTGGGGCATCAGCGCCA 1061
DB 579 TGGATAGTGCAGGGTGGGCGGCGCCCTGCGCCCGCCAGAGTAATCTGGGGCATCAGCGCCA 638
QY 1062 CGTGCTACCGCAGCGGGCGGCGCATGAGAGGGCGCGCGCCCACTACAGCAGGTATCG 1121
DB 639 CGTGCTACCGCAGCGGGCGGCGCATGAGAGGGCGCGCGCCCACTACAGCAGGTATCG 698
QY 1122 GCCACTACCGCGGGTCTCTCTCCAGCAGCAGAGCAGTGGCGCGCCCTCTCTGCTGG 1181
DB 699 GCCACTACCGCGGGTCTCTCTCCAGCAGCAGAGCAGTGGCGCGCCCTCTCTGCTGG 758
QY 1182 AGGGGACCCGGTCCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 1241
DB 759 AGGGGACCCGGTCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 818
QY 1242 AAGAGAAGGTAACAGAAAGGACACCCCTCTTAGGGTCCCGAGGGGGCGGGTGGGG 1301
DB 819 AAGAGAAGGTAACAGAAAGGACACCCCTCTTAGGGTCCCGAGGGGGCGGGTGGGG 878
QY 1302 CTGCGTAGGTGAAAGGCAG 1321
DB 879 CTGCGTAGGTGAAAGGCAG 898

RESULT 11

US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Ganavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Wonsay, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205, 823
; PRIOR FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341,746
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362,158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412

Query Match 60.6%; Score 800; DB 15; Length 1141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 CGGAGCTGGAGTTTGTTCAGATCATCATCTGTGTGGTGATGATGGTGTGTTGGTGG 581
DB 100 CGGAGCTGGAGTTTGTTCAGATCATCATCTGTGTGGTGATGATGGTGTGTTGGTGG 159
QY 582 TGATACGTGCTGCTGAGCACTACAAGTGTCTGCACGGTCTCTTCATCAGCGGCGACA 641
DB 160 TGATACGTGCTGCTGAGCACTACAAGTGTCTGCACGGTCTCTTCATCAGCGGCGACA 219
QY 642 GCAGGGGCGGAGGAGAGATGCCCTGTCTCTCAGAGGATGCTGTGTGGCCCTTCGAGA 701
DB 220 GCAGGGGCGGAGGAGAGATGCCCTGTCTCTCAGAGGATGCTGTGTGGCCCTTCGAGA 279
QY 702 GCACAGTGTTCAGCAACGGAATCCAGAGCGCGAGGTCTACGCCCGCTCGGCCACCG 761
DB 280 GCACAGTGTTCAGCAACGGAATCCAGAGCGCGAGGTCTACGCCCGCTCGGCCACCG 339
QY 762 ACCGCTTGGCGCTGCGCCCTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCAGCGCACCT 821
DB 340 ACCGCTTGGCGCTGCGCCCTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCAGCGCACCT 399
QY 822 ATCCGTACCTGACAGCAGAGATCGAAGTGCACCCACCACTCTCGTGTCTCAGCGGAGG 881
DB 400 ATCCGTACCTGACAGCAGAGATCGAAGTGCACCCACCACTCTCGTGTCTCAGCGGAGG 459
QY 882 AGCCCCACCTTACAGGGCCCTGCGACCCCTCCAGCTTCGGGACCCCGAGCAGAGTGG 941
DB 460 AGCCCCACCTTACAGGGCCCTGCGACCCCTCCAGCTTCGGGACCCCGAGCAGAGTGG 519
QY 942 AACTGAACCGGGAGTGGTGGCGGCACCCCAACAGAACCATCTTCGACAGTGACCTGA 1001
DB 520 AACTGAACCGGGAGTGGTGGCGGCACCCCAACAGAACCATCTTCGACAGTGACCTGA 579
QY 1002 TGGATAGTGCAGAGTGGGCGGCGCCCTGCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCCA 1061
DB 580 TGGATAGTGCAGAGTGGGCGGCGCCCTGCGCCCGCCAGCAGTAATCTCGGGCATCAGCGCCA 639
QY 1062 CGTGCTACCGCAGCGGGCGGCGCATGAGGGGCGCGCGCCCACTACAGCAGGTATCG 1121
DB 640 CGTGCTACCGCAGCGGGCGGCGCATGAGGGGCGCGCGCCCACTACAGCAGGTATCG 699
QY 1122 GCCACTACCGGGGTCTCTCTCCAGCAGCAGAGCAGTGGCGCGCCCTCTCTTGTGG 1181
DB 700 GCCACTACCGGGGTCTCTCTCCAGCAGCAGAGCAGTGGCGCGCCCTCTCTTGTGG 759
QY 1182 AGGGGACCCGGTTCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 1241
DB 760 AGGGGACCCGGTTCACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 819
QY 1242 AAGAGAAGGTAACAGAAAGGACACCCCTCTTAGGGTCCCGAGGGGGCGGGTGGGG 1301
DB 820 AAGAGAAGGTAACAGAAAGGACACCCCTCTTAGGGTCCCGAGGGGGCGGGTGGGG 879
QY 1302 CTGCGTAGGTGAAAGGCAG 1321
DB 880 CTGCGTAGGTGAAAGGCAG 899

RESULT 12

US-10-301-822-208
; Sequence 208, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
; APPLICANT: Millennium Pharmaceuticals, Inc.
; APPLICANT: Berger, Allison
; APPLICANT: Guillemette, Tracy L.
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.

Query Match	60.6%;	Score 800;	DB 15;	Length 1141;
Best Local Similarity	100.0%;	Prod. No. 0;		
Matches 800;	Conservative	0;	Mismatches 0;	Indels 0;
Qy	522	CGGAGCTGGAGCTTTGTTTCAGATCATCATCTGTGGTGTGATCATGTGATGCTGTGGTGG	581	
Db	100	CGGAGCTGGAGCTTTGTTTCAGATCATCATCTGTGGTGTGATGATGTGATGTGTGGTGG	159	
Qy	582	TGATCAGTGTGCTGTGAGCCATCTACAAGCTGTGTGCACGTCTCTTCATCAGCCGGCACA	641	
Db	160	TGATCAGTGTGCTGTGAGCCATCTACAAGCTGTGTGCACGTCTCTTCATCAGCCGGCACA	219	
Qy	642	GCCAGGGCGGAGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGA	701	
Db	220	GCCAGGGCGGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGGCCCTCGGAGA	279	
Qy	702	GCA CAGTGT CAGGCAA CGGAATCCAGAGCGCAGGCTCTAGCCGCCCTCGGCCCAACCG	761	
Db	280	GCA CAGTGT CAGGCAA CGGAATCCAGAGCGCAGGCTCTAGCCGCCCTCGGCCCAACCG	339	
Qy	762	ACGCCCTGGCGTGC CGGCCCTTGCCCCAGCGGGAGCGTTTCCACCGCTTCCAGCCCACT	821	
Db	340	ACGCCCTGGCGTGC CGGCCCTTGCCCCAGCGGGAGCGTTTCCACCGCTTCCAGCCCACT	399	
Qy	822	ATCCGTACTCTCAGCACAGATCGACCTGCCACCCACCATCTCGCTCTCAGACGGGGAGG	881	
Db	400	ATCCGTACTCTCAGCACAGATCGACCTGCCACCCACCATCTCGCTCTCAGACGGGGAGG	459	
Qy	882	AGCCCCACCTACCAGGGCCCTTGACCTTCAGCTTCGGGACCCCGAGCAGAGCTGG	941	
Db	460	AGCCCCACCTACCAGGGCCCTTGACCTTCAGCTTCGGGACCCCGAGCAGAGCTGG	519	
Qy	942	AACTGAACCGGGAGTCTGGTGGCGGCACCCCCAAACAGAACCATCTTCGACAGTGA	1001	
Db	520	AACTGAACCGGGAGTCTGGTGGCGGCACCCCCAAACAGAACCATCTTCGACAGTGA	579	
Qy	1002	TGATAGTGCAGGCTGGGGGGCCCTTGCCCCCCAGCAGTAATCTCGGGCATCAGCGCCA	1061	
Db	580	TGATAGTGCAGGCTGGGGGGCCCTTGCCCCCCAGCAGTAATCTCGGGCATCAGCGCCA	639	
Qy	1062	CGTGCTACGGCAGCGGCGGCATGGAGGGGGCGGCCCACTCAGCGAGGTCATCG	1121	
Db	640	CGTGCTACGGCAGCGGCGGCATGGAGGGGGCGGCCCACTCAGCGAGGTCATCG	699	
Qy	1122	GCCACTACCGGGGTCTCTTTCAGGAC CAGCAGAGCAGTGGGCCCTCTCTCTCTGG	1181	
Db	700	GCCACTACCGGGGTCTCTTTCAGGAC CAGCAGAGCAGTGGGGCCCTCTCTCTCTGG	759	

QY 1002 TGATAGTCCAGGCTGGGGGCGCCCTTGCCTCCCGCCAGAGTAACTCGGGCATCAGCGCA 1061
DB 580 TGATAGTCCAGGCTGGGGGCGCCCTTGCCTCCCGCCAGAGTAACTCGGGCATCAGCGCA 639
QY 1062 CGTGTACCGCAGCGCGCGCGCATGAGAGGGCGCGCCACCTACAGCGAGTTCATCG 1121
DB 640 CGTGTACCGCAGCGCGCGCGCATGAGAGGGCGCGCCACCTACAGCGAGTTCATCG 699
QY 1122 GCACATACCGGGGTCTCTTCCAGCACAGACAGAGTGGCGCGCTCTCTGCTG 1181
DB 700 GCCACTACCGGGGTCTCTTCCAGCACAGACAGAGTGGCGCGCTCTCTGCTG 759
QY 1182 AGGGACCGGGTCCACACACACATCGCGCCCTTAGAGCGCAGCCATCTGAGCA 1241
DB 760 AGGGACCGGGTCCACACACACATCGCGCCCTTAGAGCGCAGCCATCTGAGCA 819
QY 1242 AAGAGAAGGATAAACAGAAAGGACCCCTCTCTAGGGTCCCGAGGGGGCGGGTGGG 1301
DB 820 AAGAGAAGGATAAACAGAAAGGACCCCTCTCTAGGGTCCCGAGGGGGCGGGTGGG 879
QY 1302 CTGCGTAGGTGAAAGGCAG 1321
DB 880 CTGCGTAGGTGAAAGGCAG 899

RESULT 14

US-10-872-972-44
; Sequence 44, Application US/10872972
; Publication No. US20040229277A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872, 972
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-972-44

Query Match 60.6%; Score 800; DB 18; Length 1850;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 CGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGTGATGATGGTGGTGG 581
DB 100 CGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGTGATGATGGTGGTGG 159
QY 582 TGATCAGTGTCTGCTGAGCCACTACAAGCTGTCTGACGGTCTTTCATCAGCCGAC 641
DB 160 TGATCAGTGTCTGCTGAGCCACTACAAGCTGTCTGACGGTCTTTCATCAGCCGAC 219
QY 642 GCCAGGGCGGAGAGAGATGCCCTGCTCCTCAGAGATGCTGTGGCCCTCGGAGA 701
DB 220 GCCAGGGCGGAGAGAGATGCCCTGCTCCTCAGAGATGCTGTGGCCCTCGGAGA 279
QY 702 GCACAGTGTCTGAGCAACGGAATCCAGAGCGCAGGCTCTAGCGCCGCTCGGCCACCG 761
DB 280 GCACAGTGTCTGAGCAACGGAATCCAGAGCGCAGGCTCTAGCGCCGCTCGGCCACCG 939

QY 762 ACGCCTGCGCTGCGCGCTTGGCCAGGGGAGCGCTTCCACCGCTTCCAGCCACCT 821
DB 340 ACGCCTGCGCTGCGCGCTTGGCCAGGGGAGCGCTTCCACCGCTTCCAGCCACCT 399
QY 822 ATCCGTACCTGAGCAGCAGATCGACTGCGCACCCACCATCTCGCTGTTCAGAGCGGAGG 881
DB 400 ATCCGTACCTGAGCAGCAGATCGACTGCGCACCCACCATCTCGCTGTTCAGAGCGGAGG 459
QY 882 AGCCCCACCTTACAGAGGGCGCTGACCTTCAGTTCGGGACCCCGAGCAGCAGTGG 941
DB 460 AGCCCCACCTTACAGAGGGCGCTGACCTTCAGTTCGGGACCCCGAGCAGCAGTGG 519
QY 942 AACTGAACCGGAGTGGTGGCGCACCCCAAGAGACCATCTTCGACAGTGACCTGA 1001
DB 520 AACTGAACCGGAGTGGTGGCGCACCCCAAGAGACCATCTTCGACAGTGACCTGA 579
QY 1002 TGATAGTCCAGGCTGGGGCGCGCTGCGCGCCCGAGAGTAACTCGGGCATCAGCGCCA 1061
DB 580 TGATAGTCCAGGCTGGGGCGCGCTGCGCGCCCGAGAGTAACTCGGGCATCAGCGCCA 639
QY 1062 CGTGTACCGCAGCGCGCGCATGAGAGGGCGCGCGCCACCTTACAGCGAGTTCATCG 1121
DB 640 CGTGTACCGCAGCGCGCGCATGAGAGGGCGCGCGCCACCTTACAGCGAGTTCATCG 699
QY 1122 GCACATACCGGGGTCTCTTCCAGCACAGCAGAGTGGCGCGCTCTCTGCTG 1181
DB 700 GCACATACCGGGGTCTCTTCCAGCACAGCAGAGTGGCGCGCTCTCTGCTG 759
QY 1182 AGGGACCGGGTCCACACACACATCGCGCCCTTAGAGCGCAGCCATCTGAGCA 1241
DB 760 AGGGACCGGGTCCACACACACATCGCGCCCTTAGAGCGCAGCCATCTGAGCA 819
QY 1242 AAGAGAAGGATAAACAGAAAGGACCCCTCTCTAGGGTCCCGAGGGGGCGGGTGGG 1301
DB 820 AAGAGAAGGATAAACAGAAAGGACCCCTCTCTAGGGTCCCGAGGGGGCGGGTGGG 879
QY 1302 CTGCGTAGGTGAAAGGCAG 1321
DB 880 CTGCGTAGGTGAAAGGCAG 899

RESULT 15

US-10-872-991-44
; Sequence 44, Application US/10872991
; Publication No. US20040242860A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872, 991
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-991-44

Query Match 60.6%; Score 800; DB 18; Length 1850;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 800; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 522 CGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGTGATGATGGTGGTGG 581

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 18:35:57 ; Search time 4154.91 Seconds
(without alignments)
12102.031 Million cell updates/sec

Title: US-09-934-249-1
Perfect score: 1321
Sequence: 1 cgaccgcgtctcgagcgca.....ctgcgtaggtgaaagcgag 1321

Scoring table:
OLIGO NUC
Gapop 60.0 , Gapext 60.0

Searched: 34239544 seqs, 19032134700 residues

Word size : 0

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	741	56.1	901	3	CR612083 full-leng
2	632	47.8	1046	5	BM922276 AGENCOURT
3	614	46.5	967	5	BQ641849 AGENCOURT
4	568	43.0	916	5	BQ954555 AGENCOURT
5	558	42.2	609	5	BQ636742 hdl3h06.y
6	550	41.6	551	4	BM141979 if25all.y
7	536	40.6	605	7	CV028567 7115 Full
8	533	40.3	850	1	AL558881 AL558881
9	518	39.2	729	5	BQ575741 UI-H-EZ1-
10	511	38.7	850	5	BU602918 AGENCOURT
11	497	37.6	890	5	BQ690750 AGENCOURT
12	474	35.9	572	5	EX641317 DKF2p86K
13	471	35.7	1068	5	BU527705 AGENCOURT
14	468	35.4	655	5	BQ691705 AGENCOURT
15	450	34.1	964	5	BU859860 AGENCOURT
16	449	34.0	945	5	BU539219 AGENCOURT
17	445	33.7	782	5	BQ015170 UI-H-ED1-
18	442	33.5	602	6	CA431191 UI-H-FG1-
19	442	33.5	780	9	AY419334 Homo sapi
20	441	33.4	461	4	BM712680 UI-E-EJ0-
21	437	33.1	633	4	BM714472 UI-E-EJ0-
22	428	32.4	588	5	BU624784 UI-H-FG1-
23	425	32.2	897	1	AL558882 AL558882
24	424	32.1	1038	1	AL517150 AL517150

25	422	31.9	844	5	BQ686793 AGENCOURT
26	422	31.9	938	5	BU157842 AGENCOURT
27	422	31.9	952	5	BU157959 AGENCOURT
28	422	31.9	1280	5	BQ691500 AGENCOURT
29	417	31.6	559	2	BE855409 7g13f05.x
30	417	31.6	629	5	BU730650 UI-E-C11-
31	406	30.7	1400	4	BM559329 AGENCOURT
32	401	30.4	730	4	BM677602 UI-E-B01-
33	399	30.2	626	5	BM974296 UI-CF-EC1
34	395	29.9	544	7	CN296134 170006001
35	393	29.8	728	5	BU683523 UI-CF-EC1
36	390	29.5	973	5	BU169156 AGENCOURT
37	383	29.0	570	5	BQ575582 UI-H-EZ1-
38	377	28.5	563	6	CB049800 NISC_gj13
39	365	27.6	552	4	BM713900 UI-E-EJ0-
40	358	27.1	1127	5	BU174654 AGENCOURT
41	348	26.3	646	5	BU859841 AGENCOURT
42	338	25.6	867	5	BX362396 BX362396
43	331	25.1	899	5	BU196912 AGENCOURT
44	327	24.8	547	4	BM676516 UI-E-EJ0-
45	324	24.5	613	4	BG680325 602629217

ALIGNMENTS

RESULT 1
CR612083
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLES
JOURNAL
REMARK
REFERENCE
AUTHORS
TITLES
JOURNAL
COMMENT
FEATURES
ORIGIN
Query Match
Best Local Similarity
Matches
Mismatches
Indels
Gaps

CR612083 901 bp mRNA linear HTC 21-JUL-2004
full-length cDNA clone CS0DJ015YF12 of T cells (Jurkat cell line)
Cot 10-normalized of Homo sapiens (human).
CR612083.1 GI:50492890
HTC; CDSLT CDNA.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang, Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Faraday Avenue
2 (bases 1 to 901)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
Location/Qualifiers
1. .901
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DJ015YF12"
/tissue type="T cells (Jurkat cell line) Cot
10-normalized"
/plasmid="pCMVSPORT_6"

QY 581 GTGATCAGTGGCTGCTGAGCCACTCAAGCTCTCTGACGGTCTTCATCAGCGGCAC 640
|||||


```
QY 1007 AGTGCAGGCTGGCGGCGCCCTGCCCCCAGCAGTAACCTCGGGCATCAGCGCCACGTGC 1066
|||||
Db 661 AGTGCAGGCTGGCGGCGGNCCTGCCCCCAGCAGTAACCTCGGGCATCAGCGCCACGTGC 720
|||||
QY 1067 TACGCGAGCGCGCG 1080
|||||
Db 721 TACGCGAGCGCGCG 734
|||||

RESULT 3
BQ641849
LOCUS
DEFINITION BQ641849 967 bp mRNA linear EST 15-JUL-2002
AGENCOURT 8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
5', mRNA sequence.
ACCESSION BQ641849
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Homo sapiens (human)
REFERENCE
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
TITLE NIH-MGC http://mgi.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC2493 row: 9 column: 18
High quality sequence stop: 571.
Location/Qualifiers
1. 967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/tissue_type="pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH MGC 43"
/notes="Organ: eye; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGCCGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library. |"

ORIGIN
Query Match 46.5%; Score 614; DB 5; Length 967;
Best Local Similarity 99.7%; Pred. No. 2.6e-291;
Matches 714; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 524 GAGCTGGAGTTTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATGATG 593
|||||
Db 1 GAGCTGGAGTTTTCAGATCATCATCATCGTGGTGTGATGATGATGATGATGATGATG 60
|||||

QY 584 ATCACGTGCTGTGAGCAGCTACAGCTCTGTGACGGTCTTCATCAGCGGCACAGC 643
|||||
Db 61 ATCACGTGCTGTGAGCAGCTACAGCTCTGTGACGGTCTTCATCAGCGGCACAGC 120
|||||

QY 644 CAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAGGATGCTGTGGCCCTCGGAGAGC 703
|||||
Db 121 CAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAGGATGCTGTGGCCCTCGGAGAGC 180
|||||

QY 704 ACAGTGTACGCAACGGAATCCAGAGCCGAGGTCTAGCCCGCGCTCGGCCACCGAC 763
|||||
```

```
Db 181 ACAGTGTACGCAACGGAATCCAGAGCCGAGGTCTAGCCCGCGCTCGGCCACCGAC 240
QY 764 CGCTTGCGCGTGCCTGCGCCCTGCGCCAGCGGAGCGCTTCCACCGCTTCAGAGCCACCTAT 823
Db 241 CGCTTGCGCGTGCCTGCGCCCTGCGCCAGCGGAGCGCTTCCACCGCTTCAGAGCCACCTAT 300
QY 824 CGGTACCTGCAGCAGAGATCGACCTGCGCCAGCCACCATCTCGCTGTTCAGACGGGAGGAG 883
Db 301 CGGTACCTGCAGCAGAGATCGACCTGCGCCAGCCACCATCTCGCTGTTCAGACGGGAGGAG 360
QY 884 CCCCCACCTTACCAGGGCGCCCTGCACCTTCCAGCTTTCGGGACCCCGAGCAGCAGCTGGAA 943
Db 361 CCCCCACCTTACCAGGGCGCCCTGCACCTTCCAGCTTTCGGGACCCCGAGCAGCAGCTGGAA 420
QY 944 CTGAACCGGGAGTGGTGGCGGACCCCCCAACAGAACCATCTTCACAGTGCCTGATG 1003
Db 421 CTGAACCGGGAGTGGTGGCGGACCCCCCAACAGAACCATCTTCACAGTGCCTGATG 480
QY 1004 GATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGCAGTAACCTCGGGCATCAGCGCCACG 1063
Db 481 GATAGTGCAGGCTGGGCGGCGCCCTGCGCCAGCAGTAACCTCGGGCATCAGCGCCACG 540
QY 1064 TGCTACGGCAGCGCGCGGCGCATGAGGGGCGCGCCCGCCACCTTACAGCGAGGTTCATCGGC 1123
Db 541 TGCTACGGCAGCGCGCGGCGCATGAGGGGCGCGCGCCCGCCACCTTACAGCGAGGTTCATCGGC 600
QY 1124 CACTACCGGGGTCCTCTTCCAGACACAGAGAGAGAGTGGGCGCGCTCTCTTGTGGAG 1183
Db 601 CACTACCGGGGTCCTCTTCCAGACACAGAGAGAGAGTGGGCGCGCTCTCTTGTGGAG 660
QY 1184 GGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGAGCCATCTCGAG 1239
Db 661 GGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGAGCCATCTCGAG 716

RESULT 4
BQ954555
LOCUS
DEFINITION BQ954555 916 bp mRNA linear EST 21-AUG-2002
AGENCOURT 8825282 Lupeki_sciatic_nerve Homo sapiens cDNA clone
IMAGE:6204609 5', mRNA sequence.
ACCESSION BQ954555
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupeki
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLC13626 row: c column: 10
High quality sequence stop: 669.
Location/Qualifiers
1. 916
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6204609"
/sex="male"
/tissue_type="sciatic nerve"
/dev_stage="adult, 70 yr"
/lab_host="DH10B"
/clone_lib="Lupeki_sciatic_nerve"
```


QY 931 GCAGCAGTGAACCTGACCGGAGTGGTGGCGCACCCCAACAGAACCATCTTCGA 990
 Db 301 GCAGCAGTGAACCTGACCGGAGTGGTGGCGCACCCCAACAGAACCATCTTCGA 360
 QY 991 CAGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCAGCAGTAACCTCGG 1050
 Db 361 CAGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCAGCAGTAACCTCGG 420
 QY 1051 CATCAGGCCACGTGTCAGCGAGCGGGCGCATGAGAGGGCGCGGCCACCTACAG 1110
 Db 421 CATCAGGCCACGTGTCAGCGAGCGGGCGCATGAGAGGGCGCGGCCACCTACAG 480
 QY 1111 CGAGGTATCGGCGACCTACCGGGGCTCTCTTCCAGCACACGAGCAGTGGGGCGCC 1170
 Db 481 CGAGGTATCGGCGACCTACCGGGGCTCTCTTCCAGCACACGAGCAGTGGGGCGCC 540
 QY 1171 CTCCTTCTGAGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGC 1230
 Db 541 CTCCTTCTGAGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGCGCAGC 600
 QY 1231 CATCTGGAG 1239
 Db 601 CATCTGGAG 609

RESULT 6

BM141979
 LOCUS BM141979.1 GI:17152046
 DEFINITION if25all.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
 cDNA clone IMAGE:5677341 5' similar to TR:Q9UUD3 Q9UUD3 D0718J7.1
 // mRNA sequence.

ACCESSION

VERSION BM141979.1
 KEYWORDS EST.
 SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 551)

REFERENCE

AUTHORS Lemishka, I., Seearce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, L., Marra, M., Page, D., Wyllie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritter, B., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagareishvili, R.,
 Williams, T., Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

TITLE

JOURNAL Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 COMMENT Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138

Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohph.harvard.edu

Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center For information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu) This sequence now available from the IMAGE
 consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 429.
 Location/Qualifiers

FEATURES

source

1..551
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5677341"
 /sex="Both"
 /tissue_type="Islets of Langerhans"
 /dev_stage="Adult"
 /lab_host="DH10B"
 /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"

/notes="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
 Site_2: Sal 1; Starting library constructed using
 SuperScript Plasmid Library kit (Life Technologies). cDNA
 made by oligo-dT priming. Size-selected by column
 fractionation; average insert size 1.08 kb. Library was
 amplified once on solid support and plasmid DNA from
 method #4 from Bonaldo, Lennon, and Soares 1996 Genome
 Research 6:791-806; 0.5 microgram single-stranded library
 plasmid DNA was mixed with 5 micrograms PCR product
 representing library inserts and hybridized to an EcoT of
 20. Single-stranded (unhybridized) plasmids were isolated
 by hydroxyapatite chromatography and used to make this
 library."

ORIGIN

Query Match 41.6%; Score 550; DB 4; Length 551;
 Best Local Similarity 100.0%; Pred. No. 1e-259;
 Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 714 GCAACGGAATCCAGAGCCGAGGTCTAGCCCCCGCTCGGCCACCGACCGCTGGCCG 773
 Db 1 GCAACGGAATCCAGAGCCGAGGTCTAGCCCCCGCTCGGCCACCGACCGCTGGCCG 60
 QY 774 TCGCGCCCTTCGCCAGCGGAGGGCTTCCACCGCTTCAGGCCACCTATCCGTACTGCG 833
 Db 61 TCGCGCCCTTCGCCAGCGGAGGGCTTCCACCGCTTCAGGCCACCTATCCGTACTGCG 120
 QY 834 AGCAGCAGATCGACCTCGCCACCCACCATCTCGTGTGCAGACGGGAGAGCCCCACCT 893
 Db 121 AGCAGCAGATCGACCTCGCCACCCACCATCTCGTGTGCAGACGGGAGAGCCCCACCT 180
 QY 894 ACCAGGGCCCTGTCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCTGAACCGGG 953
 Db 181 ACCAGGGCCCTGTCACCCCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACCTGAACCGGG 240
 QY 954 AGTCGGTGGCGGACCCCAACAGAACCATCTTCGACAGTACCTGATGATAGTGCCA 1013
 Db 241 AGTCGGTGGCGGACCCCAACAGAACCATCTTCGACAGTACCTGATGATAGTGCCA 300
 QY 1014 GGTGGGGCGCCCTGCGCCCCCAGCAGTAACCTCGGCGCATCAGCGCCACCTGCTACGGCA 1073
 Db 301 GGTGGGGCGCCCTGCGCCCCCAGCAGTAACCTCGGCGCATCAGCGCCACCTGCTACGGCA 360
 QY 1074 GCGCGCGGCGCATGAGAGGGCGCCGCCCACTACAGCGAGGTGTCATCGGCCACTTACCCGG 1133
 Db 361 GCGCGCGGCGCATGAGAGGGCGCCGCCCACTACAGCGAGGTGTCATCGGCCACTTACCCGG 420
 QY 1134 GGTCTCTTCAGACACCGAGCAGAGTGGGGCGCCCTCTTGTGTGGAGGGAGCCCGGC 1193
 Db 421 GGTCTCTTCAGACACCGAGCAGAGTGGGGCGCCCTCTTGTGTGGAGGGAGCCCGGC 480
 QY 1194 TCCACACACACATCGCGCCCTTAGAGAGCCGACCATCTCGAGCAAGAGAGGATA 1253
 Db 481 TCCACACACACATCGCGCCCTTAGAGAGCCGACCATCTCGAGCAAGAGAGGATA 540
 QY 1254 AACAGAAAGG 1263
 Db 541 AACAGAAAGG 550

RESULT 7

CV028567
 LOCUS CV028567 605 bp mRNA linear EST 20-AUG-2004
 DEFINITION 7115 Full length cDNA from the Mammalian Gene Collection Homo
 sapiens cDNA 5' similar to BC015918, mRNA sequence.
 ACCESSION CV028567
 VERSION CV028567.1 GI:51486652
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

REFERENCE
AUTHORS
  Rual,J.F., Hirozane-Kishikawa,T., Hao,T., Bertin,N., Li,S.,
  Dricot,A., Li,N., Rosenberg,J., Lamesch,P., Vidalain,P.O.,
  Clingingsmith,T.R., Hartley,J.L., Esposito,D., Cheo,D., Moore,T.,
  Simmons,B., Sequerra,R., Bosak,S., Doucette-Stamm,L., Le Peuch,C.,
  Vandenhaute,J., Cusick,M.E., Albaladejo,J.S., Hill,D.E. and Vidal,M.
  Human Proteome Version 1.1: a Platform for Reverse Proteomics
  Genome Res. (2004) In press
  Contact: Vidal M
  Marc Vidal Laboratory
  Dana Farber Cancer Institute
  1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
  Tel: 617 632 5180
  Fax: 617 632 5739
  Email: Marc.Vidal@dfci.harvard.edu
  ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned ORF
  results from a PCR reaction using an MGC full-length cDNA as
  template DNA and ORF specific primers
  PCR Primers
  FORWARD: ATGATGGTATGGTGGTG
  BACKWARD: TAGAGAGGTGCTCTTCTGT
  Insert Length: 605 Std Error: 45.00
  Plate: 11020 row: 10 Column: D
  Seq primer: ACTGGCGTGTCTTACACGTCTGACTGGGAAAC
  High quality sequence start: 11
  High quality sequence stop: 604
  POLYA=No.

FEATURES
  source
    Location/Qualifiers
      1..605
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /tissue_type="mixed"
        /clone_lib="Full Length cDNA from the Mammalian Gene
        Collection"
        /note="Vector: mixed; The ORFs were PCR amplified from the
        MGC (Mammalian Gene Collection) as of April 2004 and
        cloned by recombinational Gateway cloning into pDONR223
        Donor vector. Reference : MGC (Mammalian Gene Collection)
        Program Team, Generation and Initial Analysis of more than
        15,000 Full-Length Human and Mouse cDNA Sequences. FNAS,
        2002, 99(26), 16899-16903"

ORIGIN
  Query Match 40.6%; Score 536; DB 7; Length 605;
  Best Local Similarity 99.8%; Pred. No. 8.1e-253;
  Matches 586; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 577 GGTGGTATCAGTGTCTGTGAGCCACTACAGCTGTGTGACGGTCTTTCATCAGCGG 636
DB 15 GGTGGTATCAGTGTCTGTGAGCCACTACAGCTGTGTGACGGTCTTTCATCAGCGG 74
QY 637 GCACAGCGCGGCGGAGGAGAGAGTGCCTGTCTCAGAGGATGCTGTGGCCCTC 696
DB 75 GCACAGCGCGGCGGAGGAGAGAGTGCCTGTCTCAGAGGATGCTGTGGCCCTC 134
QY 697 GGAGAGCAGTGTCTGAGCAACCGAATCCAGAGCGCGAGGTCTAGCCCGCGCTCGGCC 756
DB 135 GGAGAGCAGTGTCTGAGCAACCGAATCCAGAGCGCGAGGTCTAGCCCGCGCTCGGCC 194
QY 757 CACCGACCGCTGGCGGTGGCGCCCTTCGCCAGCGGAGCGGTTCCAGCGTTCAGCG 816
DB 195 CACCGACCGCTGGCGGTGGCGCCCTTCGCCAGCGGAGCGGTTCCAGCGTTCAGCG 254
QY 817 CACTATCCGTACTCTGAGCAGCAGAGATCGACCTGCGCCACCCACCATCTGCTGTGACAGG 876
DB 255 CACTATCCGTACTCTGAGCAGCAGAGATCGACCTGCGCCACCCACCATCTGCTGTGACAGG 314
QY 877 GGAGAGCGCCCGCCACCTTACAGGGCCCTGTGACCCCTCCAGCTTCGGGACCCCGAGCAGCA 936
DB 315 GGAGAGCGCCCGCCACCTTACAGGGCCCTGTGACCCCTCCAGCTTCGGGACCCCGAGCAGCA 374
QY 937 GCTGGAAGTGAACCGGGAGTCTGGTGGCGCGACCCCGCCAAACAGAACCATCTTCGACAGTGA 996

```

```

Db 375 GCTGGAACTGAACCGGAGTCTGGTGGCGACCCCGCCAAACAGAACCATCTTCGACAGTGA 434
QY 997 CTTGATGATAGTGTGAGTGTGAGTGTGGCGGCGCCCTGCGCCCGCCAGTAACTCGGGCATCAG 1056
DB 435 CTTGATGATAGTGTGAGTGTGAGTGTGGCGGCGCCCTGCGCCCGCCAGTAACTCGGGCATCAG 494
QY 1057 CGCCAGCTGCTAGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1116
DB 495 CGCCAGCTGCTAGGCGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 554
QY 1117 CATCGGCCACTACCGCGGCTCTCTCTCCAGCACACGAGCAGAGCAGTG 1163
DB 555 CATCGGCCACTACCGCGGCTCTCTCTCCAGCACACGAGCAGAGCAGTG 601

RESULT 8
AL558881/c
LOCUS
DEFINITION
  AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
  Homo sapiens cDNA clone CS0DJ015YF12 3-PRIME, mRNA sequence.
ACCESSION
  AL558881
VERSION
  AL558881.3 GI:46184268
SOURCE
  EST.
ORGANISM
  Homo sapiens (human)
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 850)
  Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  Full-length cDNA libraries and normalization
  Unpublished (2001)
  On Feb 15, 2001 this sequence version replaced gi.31283014.
  Contact: Genoscope
  Genoscope - Centre National de Séquencage
  2 rue Gaston Creneau, CP 5706 - 91057 EVRY cedex - FRANCE
  Email: segre@genoscope.cns.fr, Web : www.genoscope.cns.fr
  1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
  end enriched, double-strand cDNA was digested with Not I and cloned
  into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
  was normalized. Library was constructed by Life Technologies, a
  division of Invitrogen. This sequence belongs to sequence cluster
  9945.r
  For more information about this cluster, see
  http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06NP1&c=9945.r.
FEATURES
  source
    Location/Qualifiers
      1..850
        /organism="Homo sapiens"
        /mol_type="mRNA"
        /db_xref="taxon:9606"
        /clone="CS0DJ015YF12"
        /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
        /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
        10-NORMALIZED"
        /note="1st strand cDNA was primed with a NotI-oligo(dT)
        primer. Five prime end enriched, double-strand cDNA was
        digested with Not I and cloned into the Not I and EcoR V
        sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
  Query Match 40.3%; Score 533; DB 1; Length 850;
  Best Local Similarity 99.5%; Pred. No. 2.4e-251;
  Matches 733; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 585 TCAGTGTCTGCTGAGCAGCAGTGTGTGACGGTCTTTCATGCGCGGACAGCC 644
DB 846 TCAGTGTCTGCTGAGCAGCAGTGTGTGACGGTCTTTCATGCGCGGACAGCC 787
QY 645 AGGGCGGAGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGCCCTCGGAGAGCA 704
DB 786 AGGGCGGAGAGAGAGATGCCCTGTCTCAGAGGATGCTGTGCCCTCGGAGAGCA 727

```



```

QY 705 CAGTGTGAGGCAACGGAATCCAGAGCGGAGGTCTAGGCGCCGCTCGGCCACCGACC 764
Db 726 CAGTGTGAGGCAACGGAATCCAGAGCGGAGGTCTAGGCGCCGCTCGGCCACCGACC 667
QY 765 GCCTGGCGGTGCCGCCCTTCGCCAGCGGGAGCGCTTCCACCGCTTCAGGCCACCTATC 824
Db 666 GCCTGGCGGTGCCGCCCTTCGCCAGCGGGAGCGCTTCCACCGCTTCAGGCCACCTATC 607
QY 825 CGTACTGTGAGCAGAGATGCACTGTGCACCCACCATCTCGCTGTTCAGAGGGGAGGAGC 884
Db 606 CGTACTGTGAGCAGAGATGCACTGTGCACCCACCATCTCGCTGTTCAGAGGGGAGGAGC 547
QY 885 CCCACCTTACCGGGCCCTGCACTTCCAGCTTCGGGACCCCGAGCAGAGCTGAAC 944
Db 546 CCCACCTTACCGGGCCCTGCACTTCCAGCTTCGGGACCCCGAGCAGAGCTGAAC 487
QY 945 TGAACCGGGAGTGGTGGCGGCACCCCAACAGAACATCTTCGACAGTGACCTGATGG 1004
Db 486 TGAACCGGGAGTGGTGGCGGCACCCCAACAGAACATCTTCGACAGTGACCTGATGG 427
QY 1005 ATAGTGCAGGCTGGGCGGCCCTTGCCGCCAGAGTAATCTGGGGATCAGGCCACGT 1064
Db 426 ATAGTGCAGGCTGGGCGGCCCTTGCCGCCAGAGTAATCTGGGGATCAGGCCACGT 367
QY 1065 GCTACGCGAGCGGGCGGCATGAGAGGGCGCGCCGCCACCTACAGCAGGTATCGGCC 1124
Db 366 GCTACGCGAGCGGGCGGCATGAGAGGGCGCGCCGCCACCTACAGCAGGTATCGGCC 307
QY 1125 ACTACCGGGGTCTCTCTCCAGCAGCAGAGCAGTGGCGCCCTCTCTGCTGGAGG 1184
Db 306 ACTACCGGGGTCTCTCTCCAGCAGCAGAGCAGTGGCGCCCTCTCTGCTGGAGG 247
QY 1185 GGAACCGGGTCCACACACACATCGCGCCCTTAGAGGCGCAGCCATCTGGAGCAAAG 1244
Db 246 GGAACCGGGTCCACACACACATCGCGCCCTTAGAGGCGCAGCCATCTGGAGCAAAG 187
QY 1245 AGAAGGATAACAGAAAGGACCTCTTAGGGTCCCGAGGGGGCGGGCTGGGGCTG 1304
Db 186 AGAAGGATAACAGAAAGGACCTCTTAGGGTCCCGAGGGGGCGGGCTGGGGCTG 127
QY 1305 CGTAGGTGAAAGGCAG 1321
Db 126 CGTAGGTGAAAGGCAG 110

RESULT 9
BO575741/c
LOCUS
DEFINITION
  UI-H-EZ1-bbg-h-14-0-UI.s1 NCI_CGAP_Ch2 Homo sapiens cDNA clone
  UI-H-EZ1-bbg-h-14-0-UI 3', mRNA sequence.
ACCESSION
  BO575741
VERSION
  BO575741.1 GI:21479058
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
  Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 729)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Email: cgapbs-r@mail.nih.gov
  Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
  Orthopaedics
  cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
  cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
  DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
  Clone Distribution: Clone distribution information can be obtained
  from Dr. M. Bento Soares, bento-soares@uiowa.edu
  seq primer: M13 FORWARD
  POLYA=Yes.

```

FEATURES
source

```

Location/Qualifiers
1. .729
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="UI-H-EZ1-bbg-h-14-0-UI"
/tissue_type="Chondrosarcoma Grade II"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch2"
/notes="Organ: Left Pelvis; Vector: pT73-Pac (Pharmacia)
with a modified polylinker; Site 1: EcoR I; Site 2: Not I;
NCI CGAP_Ch2 is a normalized cDNA library containing the
following tissue(s): Chondrosarcoma Grade II. The library
was constructed according to Bonaldo, Lennon and Soares,
Genome Research, 6:791-806, 1996. First strand cDNA
synthesis was primed with an oligo-dT primer containing a
Not I site. Double stranded cDNA was ligated to an EcoR I
adaptor, digested with Not I, and cloned directionally
into pT73-Pac vector. The oligonucleotide used to prime
the synthesis of first-strand cDNA contains a library tag
sequence that is located between the Not I site and the
(dT)18 tail. The sequence tag for this library is
TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-EZ1
TAG_SEQ=ATCTAATATG"

```

ORIGIN

```

Query Match      39.2%; Score 518; DB 5; Length 729;
Best Local Similarity 99.8%; Pred. No. 6.1e-244;
Matches 568; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 753 GGGCCACCGACCGCCCTGGCGCTGCGCCCTTCGCCAGCGGAGCGCTTCACCGCTTCC 812
Db 729 GGGCCACCGACCGCTGGCGCTGCGCCCTTCGCCAGCGGAGCGCTTCACCGCTTCC 670
QY 813 AGCCCACTTATCGTACCTGACAGCAGAGATCGACTGCCACCCACCATCTCGCTGTGAG 872
Db 669 AGCCCACTTATCGTACCTGACAGCAGAGATCGACTGCCCGCCACCATCTCGCTGTGAG 610
QY 873 ACGGGAGGAGCGCCCAACCTTACAGGGCGCCCTGCACCTTCAGCTTCGGAGCCCGGAGC 932
Db 609 ACGGGAGGAGCGCCCAACCTTACAGGGCGCCCTGCACCTTCAGCTTCGGAGCCCGGAGC 550
QY 933 AGCAGCTGGAATCGAAACCGGGAGTCTGGTGGCGCACACCCCAACAGAACCATCTTCGACA 992
Db 549 AGCAGCTGGNACTGAACCGGGAGTCTGGTGGCGCGCACACCCCAACAGAACCATCTTCGACA 490
QY 993 GTGACCTGATGGATAGTGCAGGCTGGGGGGCCCTTGCCTCCCGCCAGCAGTAACCTCGGGCA 1052
Db 489 GTGACCTGATGGATAGTGCAGGCTGGGGGGCCCTTGCCTCCCGCCAGCAGTAACCTCGGGCA 430
QY 1053 TCAGCGCCACCTGCTACGAGCGGGGGGGGATGAGGGGGCGCCGCCACCTACAGCG 1112
Db 429 TCAGCGCCACCTGCTACGAGCGGGGGGGGATGAGGGGGCGCCGCCACCTACAGCG 370
QY 1113 AGGTCACTGGCCACTACCGGGGTCTCTCTTCCAGCACACAGCAGAGCAGTGGGGCGGCCCT 1172
Db 369 AGGTCACTGGCCACTACCGGGGTCTCTCTTCCAGCACACAGCAGAGCAGTGGGGCGGCCCT 310
QY 1173 CCTTGTCTGGAGGGGACCCCGCTCCACACACACATCGCGCCCTCTAGAGAGCGCAGCCA 1232
Db 309 CCTTGTCTGGAGGGGACCCCGCTCCACACACACATCGCGCCCTCTAGAGAGCGCAGCCA 250
QY 1233 TCTGGAGCAAGAGAGAGATAAACAGAAAGGACACCTCTCTTAGGGTCTCCCGAGGGGGCC 1292
Db 249 TCTGGAGCAAGAGAGAGATAAACAGAAAGGACACCTCTCTTAGGGTCTCCCGAGGGGGCC 190
QY 1293 GGGCTGGGCTCGTAGGTGMAAGGCAG 1321
Db 189 GGGCTGGGCTCGTAGGTGMAAGGCAG 161

```


(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."

ORIGIN

Query Match	37.6%;	Score 497;	DB 5;	Length 890;	
Best Local Similarity	99.8%;	Pred. No. 1.4e-233;			
Matches 547;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;	
QY	522	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATCATGTCGATGTCGTGG 581			
Db	128	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGATCATGTCGATGTCGTGG 187			
QY	582	TGATCATCGTGCCTGCTGAGCACTACAAGCTGTCTGCACGGTCTTTTCAGCCGGCACA 641			
Db	188	TGATCATCGTGCCTGCTGAGCACTACAAGCTGTCTGCACGGTCTTTTCAGCCGGCACA 247			
QY	642	GCCAGGGCGGAGGAGAGATGCCCTGCTCCTCAGAAGGATGCTGTGGCCCTCGGAGA 701			
Db	248	GCCAGGGCGGAGGAGAGATGCCCTGCTCCTCAGAAGGATGCTGTGGCCCTCGGAGA 307			
QY	702	GCACAGTGTTCAGGCAACCGGAATCCAGAGCCGCGAGGTCTACGCCCCCGCTCGGCCACCG 761			
Db	308	GCACAGTGTTCAGGCAACCGGAATCCAGAGCCGCGAGGTCTACGCCCCCGCTCGGCCACCG 367			
QY	762	ACGCCCTGGCGGTGCGCCCTTTCGCCCAGCGGGAGCGCTTCCACCGCTTTCAGGCCCACT 821			
Db	368	ACGCCCTGGCGGTGCGCCCTTTCGCCCAGCGGGAGCGCTTCCACCGCTTTCAGGCCCACT 427			
QY	822	ATCCGTACTCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTTCAGACGGGAGG 881			
Db	428	ATCCGTACTCTGCAGCAGCAGATCGACCTGCCACCCACCATCTCGCTGTTCAGACGGGAGG 487			
QY	882	AGCCCCACCTTACCCAGGGCCCCCTGCACCTTCCAGTTCGGGACCCCGAGCAGCAGCTGG 941			
Db	488	AGCCCCACCTTACCCAGGGCCCCCTGCACCTTCCAGTTCGGGACCCCGAGCAGCAGCTGG 547			
QY	942	AATCTGAACCGGGAGTCGGTGGCGCACCCGCCAACAGAACCATCTTTCGACAGTGACCTGA 1001			
Db	548	AATCTGAACCGGGAGTCGGTGGCGCACCCGCCAACAGAACCATCTTTCGACAGTGACCTGA 607			
QY	1002	TGGATAGTGCAGGCTGGGCGGCCCTTGGCCCCCGCCAGCAGTAACCTCGGGGATCAGCGCCA 1061			
Db	608	TGGATAGTGCAGGCTGGGCGGCCCTTGGCCCCCGCCAGCAGTAACCTCGGGGATCAGCGCCA 667			
QY	1062	CGTGCTAC 1069			
Db	668	CGTGCTAC 675			

RESULT 12	572 bp	linear	EST 04-SEP-2003
BX641317			
LOCUS			
DEFINITION	572 bp mRNA		
	DKFZp686K23134.r1.686 (synonym: hlcc3)	Homo sapiens	CDNA clone
ACCESSION	DKFZp686K23134.5		
VERSION	1		
KEYWORDS	EST.		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		

REFERENCE	Mammalia; Euterria; Primates; Catarrhini; Hominoide; Homo.
AUTHORS	1 (bases 1 to 572) Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R. Mewes, H. W., Weil, B., Amid, C., Osanger, A., Fobo, G., Han, M. and Wiemann, S.
TITLE	EST (Poustka, A., Albert, R., Moosmayer, P., Schupp, I., Wellenreuther, R., et al.)
JOURNAL	Unpublished (2003)
COMMENT	Contact: MIPS

MIPS
Ingo] staedter Landstr 1 D-85764 Neuherberg Germany

This is the 5' sequence of the clone insert clone from S. Wiemann. Molecular Genome Analysis. German Cancer Research Center, Heidelberg, D-6900 Heidelberg, Germany

Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by DKFZ (German Cancer Research Center, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.

No si sequence available.
This clone (DRFZp686K23134) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

[illegible]

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686K23134"
/dev stage="adult"
/lab_host="DH10B"
/clone lib="686 (synonym)"
/note="Vector: pTriplex2
cDNA-collection"

```

ORIGIN

Query Match 35.9%; Score 474; DB 5; Length 572;
Best Local Similarity 99.8%; Pred. No. 3,1e-222;

Qy 670 GTCCTCAGAAGGATGCCTGTGSCCTCGGAGAGCACAGTGTGAGGGCAACGGGATCCAGA 729

Db 1 GTCCTCAGAAGGATGCCTGTGGCCCTCGGAGAGCACAGTGT CAGGCAACGGAATCCAGA 60

Qy 730 GCCGAGGTTACGCCCGCGCTCGGCCCCACCGACCGCTGGCCCGCTTGGCCCA 789

Db 61 GCCGAGGTCACGCCCGCGCTCGGCCACCGACCGCTGGCGCGTGGCGCCCTCGCCCA 120

Qy 790 GCGGAGCGCTTCCACCGCTTCCAGCCCACTATCGTACCTGCAGCACGAGATCGACT 849

D_b 121 GCGGAGCGCTTCCACCGCTTCCAGCCACCTATCGTACCTGCAGCACGAGATCGACCT 180

Qy 850 GCCACCCACCATCTCTGGTGTGATGACGCGGAGAGCCCCCA CCTTACAGGGGCCCTTGAC 909

Db 181 GCCGCCACCATCTCGCTGTGACACGGGGAGGAGCCGCCACCTACAGGGGCCCTGCAC 240

910 CCTCCAGCTTCGGGACCCCGAGCAGACGCTGGAACCTGAACCGGGAGTCGGTGGCGCGCACC 989

Db 241 C T C C A G C T T C G G G A C C C C G A G C A G C T G G A A C T G A A C C G G G A G T C G G T G G C G C A C C 300

970 CCCAACACAGAACCATCTTCGACAGTGTACTCGATGGATAGTGCAGGCTTGGGGCGGGCCCCCG 1029

DB 301 CCCAAGACCATCTTCGACAGTGCCTGATGGATAGTCCAGGCTGGGGGGCCCCCCTG 360

QY	1030	361	420
CCCCCAGCAGTAACTCGGGGATCAGCGCCACGTCGTACGGGAGCGCCGGGGCGCATGGGA	CCCCCAGCAGTAACTCGGGGATCAGCGCCACGTCGTACGGGAGCGCCGGGGCGCATGGGA	CCCCCAGCAGTAACTCGGGGATCAGCGCCACGTCGTACGGGAGCGCCGGGGCGCATGGGA	

DD	361	CCCCCCCCCAGGCAAGTAACTCGGGGATCATGCGGCAACGCTGTCATCGGCAAGCGCGCGCGCGCAAGCA	420
DD			
QV	1090	GGGGGGGGCGGCGCCACTCAAGAGAGGAGTTCATGGCGCCACTACCGGGGCTCTCTCTCTCCAGCA	1149

[illegible]

22
121
QV 1150 CCAGCAGAGCAGTGGGCGCCCTCTTGCTGGAGGGGACCCGGCT 1194

Db

481 CCAGCAGACGAGTGGGCGCCCTCTTGCTGGAGGGGACCCGGCT 525

RESULT, T 13

BU527705

LOCUS

DEFINITION

ACCESSION

VERSION
KEYWORDS

KEYWORDS
COLLAPSE

SOURCE
ORGANISM

NOTES

```
REFERENCE 1 (bases 1 to 1068)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2700 row: k column: 15
High quality sequence stop: 468.

FEATURES
source
1..1068
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6537543"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cdna made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 35.7%; Score 471; DB 5; Length 1068;
Best Local Similarity 100.0%; Pred. No. 9.1e-221;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 GGGAAAGCTAGCGCAGAGGCTCAGCCCGCGGCGAGCGCGCGCTGCCAGGCCAT 151
Db 21 GGGAAAGCTAGCGCAGAGGCTCAGCCCGCGGCGAGCGCGCGCTGCCAGGCCAT 80

Qy 152 TTTCGGAGCCAGCCCGCGGCGCTGCCAGCGCCCGCGGCGCTGCCAGGCCAGCGCGG 211
Db 81 TTTCGGAGCCAGCCCGCGGCGCTGCCAGCGCCCGCGGCGCTGCCAGGCCAGCGCGG 140

Qy 212 GGGCGCGAGCGAGCGCGGCTCCCGCGACTGAGCCCGCGGCGCGCGCGCTGCCAGGCCAG 271
Db 141 GGGCGCGAGCGAGCGCGGCTCCCGCGACTGAGCCCGCGGCGCGCGCGCTGCCAGGCCAG 200

Qy 272 CGACCCGAGCCCGCGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTGCCAGGCCAGCGCGG 331
Db 201 CGACCCGAGCCCGCGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTGCCAGGCCAGCGG 260

Qy 332 CCCAGCTCCGGGCGCGCGGCGCGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 391
Db 261 CCCAGCTCCGGGCGCGCGGCGCGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 320

Qy 392 CGCGCGCGCGCGCGCGGCTCCATGCCCGCTGATGGGGGTCAACAGCACCGCGCGCGCG 451
Db 321 CGCGCGCGCGCGCGGCTCCATGCCCGCTGATGGGGGTCAACAGCACCGCGCGCGCGCG 380

Qy 452 GCGCGCGCGCGCGCGGCTCCCTGCGAGTGAACGCTCTTTGTTTCAGAGC 511
Db 381 GCGCGCGCGCGCGCGGCTCCCTGCGAGTGAACGCTCTTTGTTTCAGAGC 440

Qy 512 ATGGAGATCAGCGAGCTGAGTTGTTGTTGATCATCATCATCATCATCATCATCATCATCAT 562
Db 441 ATGGAGATCAGCGAGCTGAGTTGTTGTTGATCATCATCATCATCATCATCATCATCATCAT 491

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2700 row: k column: 15
High quality sequence stop: 468.

FEATURES
source
1..1068
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6537543"
/tissue_type="epidermoid carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_101"
/notes="Organ: lung; Vector: pOTB7; Site 1: EcoRI; Site 2:
XhoI; cdna made by oligo-dt priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 35.7%; Score 471; DB 5; Length 1068;
Best Local Similarity 100.0%; Pred. No. 9.1e-221;
Matches 471; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 92 GGGAAAGCTAGCGCAGAGGCTCAGCCCGCGGCGAGCGCGCGCTGCCAGGCCAT 151
Db 21 GGGAAAGCTAGCGCAGAGGCTCAGCCCGCGGCGAGCGCGCGCTGCCAGGCCAT 80

Qy 152 TTTCGGAGCCAGCCCGCGGCGCTGCCAGCGCCCGCGGCGCTGCCAGGCCAGCGCGG 211
Db 81 TTTCGGAGCCAGCCCGCGGCGCTGCCAGCGCCCGCGGCGCTGCCAGGCCAGCGCGG 140

Qy 212 GGGCGCGAGCGAGCGCGGCTCCCGCGACTGAGCCCGCGGCGCGCGCGCTGCCAGGCCAG 271
Db 141 GGGCGCGAGCGAGCGCGGCTCCCGCGACTGAGCCCGCGGCGCGCGCGCTGCCAGGCCAG 200

Qy 272 CGACCCGAGCCCGCGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTGCCAGGCCAGCGCGG 331
Db 201 CGACCCGAGCCCGCGAGCGCGGCGCGCTCCCGCGCGCGCGCGCTGCCAGGCCAGCGG 260

Qy 332 CCCAGCTCCGGGCGCGCGGCGCGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 391
Db 261 CCCAGCTCCGGGCGCGCGGCGCGAGCCCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCG 320

Qy 392 CGCGCGCGCGCGCGGCTCCATGCCCGCTGATGGGGGTCAACAGCACCGCGCGCGCGCG 451
Db 321 CGCGCGCGCGCGCGGCTCCATGCCCGCTGATGGGGGTCAACAGCACCGCGCGCGCGCG 380

Qy 452 GCGCGCGCGCGCGCGGCTCCCTGCGAGTGAACGCTCTTTGTTTCAGAGC 511
Db 381 GCGCGCGCGCGCGCGGCTCCCTGCGAGTGAACGCTCTTTGTTTCAGAGC 440

Qy 512 ATGGAGATCAGCGAGCTGAGTTGTTGTTGATCATCATCATCATCATCATCATCATCATCAT 562
Db 441 ATGGAGATCAGCGAGCTGAGTTGTTGTTGATCATCATCATCATCATCATCATCATCATCAT 491

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1068)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs-remail.nih.gov
Tissue Procurement: ATCC
cdna Library Preparation: Rubin Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2367 row: g column: 20
High quality sequence stop: 645.

FEATURES
source
1..655
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6208939"
/tissue_type="ductal carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_110"
/notes="Organ: pancreas; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; cdna made by oligo-dt priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCAGCAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 35.4%; Score 468; DB 5; Length 655;
Best Local Similarity 100.0%; Pred. No. 2.8e-219;
Matches 468; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 854 CCCACCATCTCGCTGTGAGCGGGGAGGAGCCCCCACCCTACCGGGGCCCTGCACCCCTC 913
Db 28 CCCACCATCTCGCTGTGAGCGGGGAGGAGCCCCCACCCTACCGGGGCCCTGCACCCCTC 87

Qy 914 CAGCTTCGGGACCCCGAGCAGAGCTGGAATGAACCCGGAGTGGTGGCGACACCCCA 973
Db 88 CAGCTTCGGGACCCCGAGCAGAGCTGGAATGAACCCGGAGTGGTGGCGACACCCCA 147

Qy 974 AACAGAACCATCTTCGACAGTGACTGATGATGATGATGATGATGATGATGATGATGATG 1033
Db 148 AACAGAACCATCTTCGACAGTGACTGATGATGATGATGATGATGATGATGATGATGATG 207

Qy 1034 CCCAGCAGTAATCTGGGCGATCAGCGCCACGCTGCTACGGCAGCGGGCGGCGATGAGGGG 1093
Db 208 CCCAGCAGTAATCTGGGCGATCAGCGCCACGCTGCTACGGCAGCGGGCGGCGATGAGGGG 267

Qy 1094 CCGCGCCCGACCTACAGCGAGTCACTGGCCACTACCGGGGTCTCTCTTCAGACACAG 1153
Db 268 CCGCGCCCGACCTACAGCGAGTCACTGGCCACTACCGGGGTCTCTCTTCAGACACAG 327

Qy 1154 CAGAGCAGTGGCGCGCCCTCTTGTGTGAGGGGACCGGGCTCCACACACATCGCG 1213
Db 328 CAGAGCAGTGGCGCGCCCTCTTGTGTGAGGGGACCGGGCTCCACACACATCGCG 387
```

```
QY 1214 CCCTAGAGAGCGCAGCCATCTCGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 1273
Db 388 CCCTAGAGAGCGCAGCCATCTCGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 447
QY 1274 TAGGGTCCCCCAGGGGGGCCGGGCTGGGGCTCGCTAGGTGAAAGGCAG 1321
Db 448 TAGGGTCCCCCAGGGGGGCCGGGCTGGGGCTCGCTAGGTGAAAGGCAG 495

RESULT 15
BU859860
LOCUS AGENECOURT_10442713_NIH_MGC_107_Homo_sapiens_cDNA_clone EST 16-OCT-2002
DEFINITION IMAGE:6650839 5', mRNA sequence.
ACCESSION BU859860
VERSION BU859860.1 GI:24044852
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 964)
NTH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-x@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L1CM2896 row: 1 column: 07
High quality sequence stop: 613.
FEATURES
    source
        1..964
            /organism="Homo sapiens"
            /mol_type="mRNA"
            /db_xref="taxon:9606"
            /clone="IMAGE:6650839"
            /tissue_type="adenocarcinoma, cell line"
            /lab_host="DH10B (phage-resistant)"
            /clone_lib="NIH_MGC_107"
            /note="Organ: breast; Vector: pOTB7; Site 1: EcoRI;
            Site 2: XhoI; cDNA made by oligo-dT priming.
            Directionally cloned into EcoRI/XhoI sites using the
            following 5' adaptor: GGCAGAG(G). Library constructed by
            Ling Hong in the laboratory of Gerald M. Rubin (University
            of California, Berkeley) using ZAP-cDNA synthesis kit
            (Stratagene) and Superscript II RT (Life Technologies).
            Note: this is a NIH_MGC Library."

ORIGIN
Query Match 34.1%; Score 450; DB 5; Length 964;
Best Local Similarity 100.0%; Pred. No. 2.1e-210;
Matches 450; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 872 GACGGGAGAGAGCCCCCACCCTACAGGGGCGCTGACACCTCCAGCTTCGGGACCCCGAG 931
Db 35 GACGGGAGAGAGCCCCCACCCTACAGGGGCGCTGACACCTCCAGCTTCGGGACCCCGAG 94
QY 932 CAGCAGCTGGAACCTGAACCGGGAGTCGGTGGCGCACCCCAACAGAACCATCTTCGAC 991
Db 95 CAGCAGCTGGAACCTGAACCGGGAGTCGGTGGCGCACCCCAACAGAACCATCTTCGAC 154
QY 992 AGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCAGCAGTAACCTCGGC 1051
Db 155 AGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCAGCAGTAACCTCGGC 214
QY 1052 ATCAGCCCAAGTGTACGGCAGCGGGGGCGCATGGAGGGGCGCGCCACCTACAGC 1111
```

```
Db 215 ATCAGCGCCACGTGCTACGGCAGCGGGGGCGCATGGAGGGGCGCGCCACCTACAGC 274
QY 1112 GAGGTCAATCGGCCCACTACCCCGGGGTCTCTTCCAGCAACAGCAGAGCAGTGGGCCGCC 1171
Db 275 GAGGTCAATCGGCCCACTACCCCGGGGTCTCTTCCAGCAACAGCAGAGCAGTGGGCCGCC 334
QY 1172 TCCTTCTGAGGGGAGCCCGGCTCCACCAACACACATCGCGCCCTAGAGAGCGCAGCC 1231
Db 335 TCCTTCTGAGGGGAGCCCGGCTCCACCAACACACATCGCGCCCTAGAGAGCGCAGCC 394
QY 1232 ATCTGAGCAAAAGAGAGGATTAACAGAAAGGACACCCCTCTCTAGGGTCCCCCAGGGGGGC 1291
Db 395 ATCTGAGCAAAAGAGAGGATTAACAGAAAGGACACCCCTCTCTAGGGTCCCCCAGGGGGGC 454
QY 1292 CGGGCTGGGGCTGCGTAGGTGAAAGGCAG 1321
Db 455 CGGGCTGGGGCTGCGTAGGTGAAAGGCAG 484
```

Search completed: February 19, 2005, 23:58:32
Job time : 4159.91 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 06:35:20 ; Search time 3714.3 Seconds
(without alignments)
11232.262 Million cell updates/sec

Title: US-09-934-249-3
Perfect score: 861
Sequence: 1 atgcaccgttgatgggggt.....aacagaaaggacaccctctc 861

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_htg.*
- 3: gb_in.*
- 4: gb_cm.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	861	100.0	861 6 AX392419 Sequence
2	861	100.0	1321 6 AX392417 Sequence
3	861	100.0	4839 6 CQ812357 Sequence
4	861	100.0	4839 6 AF305616 Homo sapi
5	859.4	99.8	1383 6 AX775889 Sequence
6	839.4	97.5	1061 9 BC015918 Homo sapi
7	755.2	87.7	969 6 BD272494 Secretd
8	754.2	87.6	1141 9 AF224278 Homo sapi
9	753.8	87.5	1913 6 BD272544 Secretd
10	753.6	87.5	969 6 BD272514 Secretd
11	753.6	87.5	969 6 BD272515 Secretd
12	753.6	87.5	969 6 BD272516 Secretd
13	752.8	87.4	1140 6 AR336830 Sequence
14	752.8	87.4	759 6 AR336831 Sequence
15	752.6	87.4	1085 6 AX775887 Sequence
16	752.4	87.4	759 6 BD272545 Secretd
17	752	87.3	1818 9 AY128643 Homo sapi
18	751.2	87.2	756 6 BD272495 Secretd
19	750.4	87.2	753 6 BD272534 Secretd

20	749.4	87.0	1060	9	BC080635	Homo sapi	
21	614.6	71.4	1379	10	BC036995	Mus muscu	
22	612.4	71.1	878	6	AX392428	Sequence	
23	597	69.3	600	6	CQ728942	Sequence	
24	584	67.8	895	10	BC069890	Mus muscu	
25	564.4	65.6	1265	5	AJ720618	Gallus ga	
26	546.4	63.5	61505	9	AF305426	Homo sapi	
C	27	546.4	63.5	130435	9	HS718J7	Human DNA
28	544.4	63.2	1583	6	AX593655	Sequence	
29	462.2	53.7	1713	6	BD272504	Secretd	
30	461.2	53.6	651	6	BD272505	Secretd	
31	460.6	53.5	1713	6	BD272517	Secretd	
32	460.6	53.5	1713	6	BD272518	Secretd	
33	460.6	53.5	1713	6	BD272519	Secretd	
34	458.2	53.2	648	6	BD272535	Secretd	
C	35	445.6	51.8	693	6	AX392430	Sequence
36	421	48.9	651	10	AF220208	Mus muscu	
37	417.4	48.5	812	6	BD226320	Pancreati	
38	417.4	48.5	812	6	AX011709	Sequence	
39	401.4	46.6	408	6	AX071267	Sequence	
40	400.6	46.5	673	6	AX525744	Sequence	
C	41	373.2	43.3	156698	10	AL837509	Mouse DNA
42	373.2	43.3	175847	2	AC110189	Mus muscu	
C	43	373.2	43.3	231930	2	AC134911	Mus muscu
C	44	353.6	41.1	249554	2	AC139417	Rattus no
45	353.6	41.1	258632	2	AC111878	Rattus no	

ALIGNMENTS

RESULT 1
AX392419
LOCUS AX392419 861 bp DNA linear PAT 23-MAR-2002
DEFINITION Sequence 3 from Patent WO0216416.
ACCESSION AX392419
VERSION AX392419.1 GI:19700734
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Lee,R.T., Landschulz,K.T., Kennedy,S.P., Thompson,J.F. and Turi,T.G.
TITLE Diagnosis and treatment of cardiovascular conditions
JOURNAL Patent: WO 0216416-A 3 28-FEB-2002;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US) ; PFIZER INC. (US)
FEATURES
source Location/Qualifiers
1..861
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1..>861
/notes="unnamed protein product"
/codon_start=1
/protein_id="CAD29006.1"
/db_xref="GI:19700735"
/translation="MRLMGVNSTAAAGOPNVCTCNKRSFOSMEITFEFVQI
IIIVVMVMVVITCLSHYKLSAKSFISRHSGRRRDLALSEGLWSESTVSGN
GIPEQVYAPPPTRDLAVPPAQRERFHRFQTYLYLQHEIDLPPTISLSDGEPP
YQPCYQLDRDPEQQLNRESVRAPNRTIFDSDLMSARLQDPCPPSPNSGISATC
YSGGRMEGPPPTYSVIGHYPGSSFHQOSSGPPSLLEGLRLHHTHIAPLESAAIWS
KEKDQKQHPL"

ORIGIN

Query Match 100.0%; Score 861; DB 6; Length 861;
Best Local Similarity 100.0%; Pred. No. 7.4e-137;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCGTGTGATGGGGTCAACAGACCGCGCGCGCGCGCGCGCAATGTC 60
|||||
Db 1 ATGCACCGTGTGATGGGGTCAACAGACCGCGCGCGCGCGCGCGCAATGTC 60
|||||


```
Db 1133 GGGTCTCTTCCAGCACACGAGAGAGAGTGGCGCCCTCTCTTCTGGAGGGGACCCGG 1192
Qy 781 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAAAGAGAGGAT 840
Db 1193 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAAAGAGAGGAT 1252
Qy 841 AAACAGAAAGGACACCCCTCTC 861
Db 1253 AAACAGAAAGGACACCCCTCTC 1273

RESULT 3
CQ812357
DEFINITION Sequence 109 from Patent WO2004038020.
ACCESSION CQ812357
VERSION CQ812357.1 GI:47601977
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Wittig, R., Poustka, A., Mollenhauer, J. and Schadendorf, D.
TITLE Target genes for the diagnosis and treatment of cancer
JOURNAL Patent: WO 2004038020-A 109 06-MAY-2004;
Deutsches Krebsforschungszentrum Stiftung des oeffentlichen n Rechts
(DE)
FEATURES
source Location/Qualifiers
1..4839
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
misc_feature 1..4839
/note="NM_020182"
ORIGIN
Query Match 100.0%; Score 861; DB 6; Length 4839;
Best Local Similarity 100.0%; Pred. No. 5.8e-137;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCGCTTGATGGGGGTCAACAGCAGCCGCGCCCGCGCGGGGAGCCCAATGTC 60
Db 321 ATGCACCGCTTGATGGGGGTCAACAGCAGCCGCGCCCGCGCGGGGAGCCCAATGTC 380
Qy 61 TCCTGCACGCGCAACTGCCAAACGCTCTTCTTCAGAGCATGAGATCACGGAGCTGGAG 120
Db 381 TCCTGCACGCGCAACTGCCAAACGCTCTTCTTCAGAGCATGAGATCACGGAGCTGGAG 440
Qy 121 TTTGTTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 180
Db 441 TTTGTTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGC 500
Qy 181 CTGCTGAGCCACTAACAGCTGTCTGACAGCTCTTCTTCATACGCGGCGCACAGCCAGGGGCGG 240
Db 501 CTGCTGAGCCACTAACAGCTGTCTGACAGCTCTTCTTCATACGCGGCGCACAGCCAGGGGCGG 560
Qy 241 AGGAGAGAAATGCCCTGCTCAGAGAGTGCCTGCGCCCTCGGAGAGCACAGTGTCA 300
Db 561 AGGAGAGAAATGCCCTGCTCAGAGAGTGCCTGCGCCCTCGGAGAGCACAGTGTCA 620
Qy 301 GGCACCGGAATCCAGAGCGCAGGTCTACGCGCCGCTCGGCGCCACCGACCGCTGGCC 360
Db 621 GGCACCGGAATCCAGAGCGCAGGTCTACGCGCGCTCGGCGCCACCGACCGCTGGCC 680
Qy 361 GTGCGCGCTTCGCGCCAGCGGAGCGCTTCCACGCTTCAGGCCACCTTATCCGTAACCTG 420
Db 681 GTGCGCGCTTCGCGCCAGCGGAGCGCTTCCACGCTTCAGGCCACCTTATCCGTAACCTG 740
Qy 421 CAGCAGAGATCGACCTGCCACCCACCATCTCGTGTGCACAGGGGAGGAGCCGCCACCC 480
Db 741 CAGCAGAGATCGACCTGCCACCCACCATCTCGTGTGCACAGGGGAGGAGCCGCCACCC 800
```

```
Qy 481 TACCAGGGGCCCTGCAACCTTCAGCTTCGGGACCCGAGCAGCAGCTGGAACTGAACCGG 540
Db 801 TACCAGGGGCCCTGCAACCTTCAGCTTCGGGACCCGAGCAGCAGCTGGAACTGAACCGG 860
Qy 541 GAGTCGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTGATGGATAGTGCC 600
Db 861 GAGTCGGTGGCGCACCCCAACAGAACCATCTTCGACAGTGCACCTGATGGATAGTGCC 920
Qy 601 AGGCTGGGCGGCCCTTCGCCCCCAGCAGTAAGTAACTCGGGGCATCAGCGCCACGTGCTACGGC 660
Db 921 AGGCTGGGCGGCCCTTCGCCCCCAGCAGTAAGTAACTCGGGGCATCAGCGCCACGTGCTACGGC 980
Qy 661 AGCGGGGGGCGCATGTAGAGGGGCGCGCCGCCACCTACAGCGAGGTCTATCGGCCATACCCG 720
Db 981 AGCGGGGGGCGCATGTAGAGGGGCGCGCCGCCACCTACAGCGAGGTCTATCGGCCATACCCG 1040
Qy 721 GGGTCTCTCTTCAGCAGCAGCAGCAGTGGGCGCCCTCTCTTGTGGAGGGGACCCGG 780
Db 1041 GGGTCTCTCTTCAGCAGCAGCAGCAGTGGGCGCCCTCTCTTGTGGAGGGGACCCGG 1100
Qy 781 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAAAGAGAGGAT 840
Db 1101 CTCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAAAGAGAGGAT 1160
Qy 841 AAACAGAAAGGACACCCCTCTC 861
Db 1161 AAACAGAAAGGACACCCCTCTC 1181

RESULT 4
AF305616
LOCUS Homo sapiens STAG1/PMEP1 mRNA, complete cds.
DEFINITION AF305616
ACCESSION AF305616
VERSION AF305616.1 GI:16303741
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 4839)
AUTHORS Rae, P.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
TITLE Characterization of a novel gene, STAG1/PMEP1, upregulated in
renal cell carcinoma and other solid tumors
JOURNAL Mol. Carcinog. 32 (1), 44-53 (2001)
MEDLINE 21453682
PUBMED 11568975
REFERENCE 2 (bases 1 to 4839)
AUTHORS Rae, P.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.
TITLE Direct Submission
JOURNAL Submitted (14-SEP-2000) Centre for Molecular Biotechnology,
Queensland University of Technology, 2 George St, Brisbane, QLD
4001, Australia
FEATURES
source Location/Qualifiers
1..4839
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/chrosome="20"
/map="20q13.2-q13.33"
321..1184
/notes="unknown function"
/codon_start=1
/product="STAG1/PMEP1"
/protein_id="AA116781.1"
/db_xref="GI:16303742"
/translation="MERLMGVNSTAAAGQPNVSCNKRSLFQSMETLEFVQI
IIIVVMVMVVVITCLSHYKLSARFSRHSQRRRDLASSEGCLWPSSTVSGN
GIPEQVYAPPRPTDLAVPFAORERFHFQYPLYOHEIDLPTIISLDGEPP
YQGPCTLIQRDEPQLELNRESVRAPPNTIIFDSLDMSNARLGCPFPSNSGISATC
YSGGNGMEGPPPTYSIVIGHYPGSSFPHQOOSGPPSLLELTRLHHTHIAPLESAAIWS
KEKDQKQKGPL"
```


QY	87	TTTGTTCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCATCTCGTGT	146
Db	127	TCCTCTGCCAAACACGAGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCTCGTGT	186
QY	147	GGTGATGATGGTGATGTGGTGATCACTGCTGCTGAGCCACTTACAAGCTGTCTGC	206
Db	187	GGTGATGATGGTGATGTGGTGATCACTGCTGCTGAGCCACTTACAAGCTGTCTGC	246
QY	207	AGGTCTTTTCATACGCGGCACAGCCAGGGGCGGAGAGAGATGCTCTGCTTCAGA	266
Db	247	ACGGTCTTTTCATACGCGGCACAGCCAGGGGCGGAGAGAGATGCCCTGTCTTCAGA	306
QY	267	AGGATGCCGTGCGCCCTCGGAGAGACAGTGTCAAGCAACGGATCCAGAGCGCGAGT	326
Db	307	AGATGCCCTGTGGCCCTCGGAGAGACAGTGTCAAGCAACGGATCCAGAGCGCGAGT	366
QY	327	CTACGCCCGCCCTCGGCCCAACCGACCGCCTCGCCGCTGCGCCCTTGCCCCAGCGGAGCG	386
Db	367	CTAGGCCCGCCCTCGGCCCAACCGACCGCCTGCGCCCTTGCCCCAGCGGAGCG	426
QY	387	CTTCCACGGCTTCAGAGCCACCTATTCGGTACTTCGACGACGAGATGACTGCCACCAAC	446
Db	427	CTTCCACGGCTTCAGAGCCACCTATTCGGTACTTCGACGACGAGATGACTGCCACCAAC	486
QY	447	CATCTCGCTGTCAAGCGGGAGAGCCGCCACCTTACGAGGGCCCTTGACACCTTCAGCT	506
Db	487	CATCTCGCTGTCAAGCGGGAGAGCCGCCACCTTACGAGGGCCCTTGACACCTTCAGCT	546
QY	507	TCGGGACCCCGAGAGCAGCTGGAACTGAAACCGGAGTTCGGTGGCGCACCCGCCAAACAG	566
Db	547	TCGGGACCCCGAGAGCAGCTGGAACTGAAACCGGAGTTCGGTGGCGCACCCGCCAAACAG	606
QY	567	AACCATCTTCGACAGTGAACCTGATGGATAGTGCAGAGCTGGCGGCGCCCTGCCCCCAG	626
Db	607	AACCATCTTCGACAGTGAACCTGATGGATAGTGCAGAGCTGGCGGCGCCCTGCCCCCAG	666
QY	627	CAGTAACTCGGGCATCAGCGCCACGTGTACGCGAGCGGGCGGCGCATGAGAGGGCGCGC	686
Db	667	CAGTAACTCGGGCATCAGCGCCACGTGTACGCGAGCGGGCGGCGCATGAGAGGGCGCGC	726
QY	687	GCCCACTTACAGGAGGTCATCGGCCATACCCGGGGTCTCTTTCAGGACGAGCAGAG	746
Db	727	GCCCACTTACAGGAGGTCATCGGCCATACCCGGGGTCTCTTTCAGGACGAGCAGAG	786
QY	747	CAGTGGGCGCGCCTCTTGTCTGGAGGGGACCCGGCTCCACACACACATCGCGCCCT	806
Db	787	CAGTGGGCGCGCCTCTTGTCTGGAGGGGACCCGGCTCCACACACACATCGCGCCCT	846
QY	807	AGAGAGCGGAGCCATCTCGAGCAAGAGAGGATAAACAGAAAGGACACCTCTC	861
Db	847	AGAGAGCGGAGCCATCTCGAGCAAGAGAGGATAAACAGAAAGGACACCTCTC	901
RESULT 10			
BD272514			
LOCUS			
DEFINITION			
SECRETED proteins and nucleic acids encoding them.			
ACCESSION			
BD272514.1			
VERSION			
JP 2002539773-A/23.			
KEYWORDS			
SOURCE			
Homo sapiens			
ORGANISM			
Homo sapiens			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
1 (bases 1 to 969)			
Barnes, T.M., Holtzman, D.A., Sharp, J.D. and Fraser, C.C.			
Secreted proteins and nucleic acids encoding them			
Patent: JP 2002539773-A 23 26-NOV-2002;			
MILLENNIUM PHARMACEUTICALS INC			
OS Homo sapiens (human)			
PN JP 2002539773-A/23			
PD 26-NOV-2002			


```

RESULT 11
BD272515
LOCUS          BD272515          969 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION     Secreted proteins and nucleic acids encoding them.
ACCESSION      BD272515
VERSION        BD272515.1 GI:33082283
KEYWORDS       JP 2002539773-A/24..
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 969)
AUTHORS        Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
TITLE          Secreted proteins and nucleic acids encoding them
JOURNAL        Patent: JP 2002539773-A 24 26-NOV-2002;
               MILLENNIUM PHARMACEUTICALS INC
COMMENT        OS Homo sapiens (human)
               PN JP 2002539773-A/24
               PD 26-NOV-2002
               PP 01-MAR-2000 JP 2000602247
               PR 01-MAR-1999 US 60/122458
               PI THOMAS M BARNES,DOUGLAS A HOLTZMAN,JOHN D SHARP,CHRISTOPHER C
               PI FRASER
               PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
               GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00 CC
               Secreted proteins and nucleic acids encoding them FH Key
               Location/Qualifiers
               FT CDS             Location/Qualifiers
               source            1..969
                               /organism="Homo sapiens"
                               /mol_type="genomic DNA"
                               /db_xref="taxon:9606"

ORIGIN
Query Match      87.5%; Score 753.6; DB 6; Length 969;
Best Local Similarity 99.5%; Pred. No. 1.4e-118;
Matches 756; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 102 GGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTAT 161
DB 2 GGAGATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTAT 61

QY 162 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 221
DB 62 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121

QY 222 CCGGCACAGCGAGCGGCGGAGGAGAGAGTGCCTGTCTCTCAGAAAGGATGCCTGTGGCC 281
DB 122 CCGGCACAGCGAGCGGCGGAGGAGAGAGTGCCTGTCTCTCAGAAAGGATGCCTGTGGCC 181

```

```

QY 582 TGACCTGATGATAGTCCAGGCTGGCGGCGCCCTGCCCCCAGCAGTAACCTCGGGCAT 641
DB 482 TGACCTGATGATAGTCCAGGCTGGCGGCGCCCTGCCCCCAGCAGTAACCTCGGGCAT 541

QY 642 CAGCGCCACGTGCTAGCGGAGCGGCGGCGCATGGAGGGGCGCGCCACCTACAGCGA 701
DB 542 CAGCGCCACGTGCTAGCGGAGCGGCGGCGCATGGAGGGGCGCGCCACCTACAGCGA 601

QY 702 GGTATCGGCCACTACCCGGGGTCTCTTCCTTCAGACACACCATGCGGCCCTAGAGAGCGCAGCAT 761
DB 602 GGTATCGGCCACTACCCGGGGTCTCTTCCTTCAGACACACCATGCGGCCCTAGAGAGCGCAGCAT 661

QY 762 CTTGCTGGAGGGGAGCGGCGCTCCACACACACATGCGGCCCTAGAGAGCGCAGCAT 821
DB 662 CTTGCTGGAGGGGAGCGGCGCTCCACACACACATGCGGCCCTAGAGAGCGCAGCAT 721

QY 822 CTGGAGCAAGAGAGAGATAAACAGAAAGGACACCCCTCTC 861
DB 722 CTGGAGCAAGAGAGAGATAAACAGAAAGGACACCCCTCTC 761

RESULT 12
BD272516
LOCUS          BD272516          969 bp    DNA    linear    PAT 17-JUL-2003
DEFINITION     Secreted proteins and nucleic acids encoding them.
ACCESSION      BD272516
VERSION        BD272516.1 GI:33082284
KEYWORDS       JP 2002539773-A/25.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
               Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 969)
AUTHORS        Barnes,T.M., Holtzman,D.A., Sharp,J.D. and Fraser,C.C.
TITLE          Secreted proteins and nucleic acids encoding them
JOURNAL        Patent: JP 2002539773-A 25 26-NOV-2002;
               MILLENNIUM PHARMACEUTICALS INC
COMMENT        OS Homo sapiens (human)
               PN JP 2002539773-A/25
               PD 26-NOV-2002
               PP 01-MAR-2000 JP 2000602247
               PR 01-MAR-1999 US 60/122458
               PI THOMAS M BARNES,DOUGLAS A HOLTZMAN,JOHN D SHARP,CHRISTOPHER C
               PI FRASER
               PC C12N15/09,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
               GOIN33/50,GOIN33/53,GOIN33/53,GOIN33/566,C12N15/00,C12N5/00 CC
               Secreted proteins and nucleic acids encoding them FH Key
               Location/Qualifiers
               FT CDS             Location/Qualifiers
               source            1..969
                               /organism="Homo sapiens"
                               /mol_type="genomic DNA"
                               /db_xref="taxon:9606"

ORIGIN
Query Match      87.5%; Score 753.6; DB 6; Length 969;
Best Local Similarity 99.5%; Pred. No. 1.4e-118;
Matches 756; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 102 GGAGATCAGCGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTAT 161
DB 2 GGAGATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTAT 61

QY 162 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 221
DB 62 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 121

QY 222 CCGGCACAGCGAGCGGCGGAGGAGAGAGTGCCTGTCTCTCAGAAAGGATGCCTGTGGCC 281
DB 122 CCGGCACAGCGAGCGGCGGAGGAGAGAGTGCCTGTCTCTCAGAAAGGATGCCTGTGGCC 181

```

```
QY 282 CTCGAGAGCAGTGTTCAGGCAACGGAATCCCAAGAGCCGCGAGTCTACGCCCGCGCTCG 341
Db 182 CTCGAGAGCAGTGTTCAGGCAACGGAATCCCAAGAGCCGCGAGTCTACGCCCGCGCTCG 241
QY 342 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 401
Db 242 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 301
QY 402 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 461
Db 302 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 361
QY 462 CGGGGAGAGCCGCCACCCCTACCAAGGCGCCCTGCAACCCCTCCAGCTTCGGGAGCCCGAGCA 521
Db 362 CGGGGAGAGCCGCCACCCCTACCAAGGCGCCCTGCAACCCCTCCAGCTTCGGGAGCCCGAGCA 421
QY 522 GCAGCTGGAATGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACT 581
Db 422 GCAGCTGGAATGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACT 481
QY 582 TGACCTGATGATAGTGCAGGCTGCGCGCGCCCTGCGCGCCAGCAAGTAACTCGGGCAT 641
Db 482 TGACCTGATGATAGTGCAGGCTGCGCGCGCCCTGCGCGCCAGCAAGTAACTCGGGCAT 541
QY 642 CAGCGCCAGCTGTACGGGAGCGCGCGCGCGGATGAGAGGCGCGCGCGCGCGCGCGCGCGCT 701
Db 542 CAGCGCCAGCTGTACGGGAGCGCGCGCGCGGATGAGAGGCGCGCGCGCGCGCGCGCGCGCT 601
QY 702 GGTTCATCGGCGCACTACCGCGGCTCTCTCTTCAGAGCAGCAGCAGCAGCAGCAGCAGCAG 761
Db 602 GGTTCATCGGCGCACTACCGCGGCTCTCTCTTCAGAGCAGCAGCAGCAGCAGCAGCAGCAG 661
QY 762 CTTGCTGAGGAGGAGCCCGGCTCCACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 821
Db 662 CTTGCTGAGGAGGAGCCCGGCTCCACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 721
QY 822 CTGGAGCAAGAGAGAGGATAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 881
Db 722 CTGGAGCAAGAGAGAGGATAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 781

RESULT 13
AR336830
LOCUS AR336830 1140 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 1 from patent US 6566130.
ACCESSION AR336830
VERSION AR336830.1 GI:33722680
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1140)
AUTHORS Srivastava, S., Moul, J. W., Xu, L. L. and Segawa, T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 1 20-MAY-2003;
FEATURES
    source
        location/Qualifiers
            1..1140
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
    Query Match 87.5%; Score 753.6; DB 6; Length 1140;
    Best Local Similarity 99.5%; Pred. No. 1.4e-118;
    Matches 756; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 102 GGAGATCAGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGT 161
Db 91 GGCATAGGCGGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGT 150
QY 162 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 221
Db 151 GGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 210
```

```
QY 222 CCGGCAAGCAGCCAGGCGGAGGAGAGAGATGCGCTGTCTCTCAGAGGAGTCCCTGTGGCC 281
Db 211 CCGGCAAGCAGCCAGGCGGAGGAGAGAGATGCGCTGTCTCTCAGAGGAGTCCCTGTGGCC 270
QY 282 CTGCGAGAGCAGTGTTCAGGCAACGGAATCCCAAGAGCCGCGAGTCTACGCCCGCGCTCG 341
Db 271 CTGCGAGAGCAGTGTTCAGGCAACGGAATCCCAAGAGCCGCGAGTCTACGCCCGCGCTCG 330
QY 342 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 401
Db 331 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 390
QY 402 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 461
Db 391 GCCCAGCAGCCGCTGCGCGCTGCGCGCTGCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 450
QY 462 CGGGGAGAGCCGCCACCCCTACCAAGGCGCCCTGCAACCCCTCCAGCTTCGGGAGCCCGAGCA 521
Db 451 CGGGGAGAGCCGCCACCCCTACCAAGGCGCCCTGCAACCCCTCCAGCTTCGGGAGCCCGAGCA 510
QY 522 GCAGCTGGAATGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACT 581
Db 511 GCAGCTGGAATGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACT 570
QY 582 TGACCTGATGATAGTGCAGGCTGCGCGCGCCCTGCGCGCCAGCAAGTAACTCGGGCAT 641
Db 571 TGACCTGATGATAGTGCAGGCTGCGCGCGCCCTGCGCGCCAGCAAGTAACTCGGGCAT 630
QY 642 CAGCGCCAGCTGTACGGGAGCGCGCGCGGATGAGAGGCGCGCGCGCGCGCGCGCGCGCT 701
Db 631 CAGCGCCAGCTGTACGGGAGCGCGCGCGGATGAGAGGCGCGCGCGCGCGCGCGCGCGCT 690
QY 702 GGTTCATCGGCGCACTACCGCGGCTCTCTCTTCAGAGCAGCAGCAGCAGCAGCAGCAGCAG 761
Db 691 GGTTCATCGGCGCACTACCGCGGCTCTCTCTTCAGAGCAGCAGCAGCAGCAGCAGCAGCAG 750
QY 762 CTTGCTGAGGAGGAGCCCGGCTCCACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 821
Db 751 CTTGCTGAGGAGGAGCCCGGCTCCACCAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 810
QY 822 CTGGAGCAAGAGAGAGGATAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 881
Db 811 CTGGAGCAAGAGAGAGGATAAACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 781

RESULT 14
AR336831
LOCUS AR336831 759 bp DNA linear PAT 17-AUG-2003
DEFINITION Sequence 2 from patent US 6566130.
ACCESSION AR336831
VERSION AR336831.1 GI:33722681
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 759)
AUTHORS Srivastava, S., Moul, J. W., Xu, L. L. and Segawa, T.
TITLE Androgen-regulated gene expressed in prostate tissue
JOURNAL Patent: US 6566130-A 2 20-MAY-2003;
FEATURES
    source
        location/Qualifiers
            1..759
                /organism="unknown"
                /mol_type="genomic DNA"
ORIGIN
    Query Match 87.4%; Score 752.8; DB 6; Length 759;
    Best Local Similarity 99.7%; Pred. No. 2e-118;
    Matches 754; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 106 ATCAGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGT 165
Db 1 ATGCGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGTGGTGGTGGTGGTGGTGGTGGTGGT 60
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 00:48:19 ; Search time 460.884 Seconds
(without alignments)
11058.969 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861

Sequence: 1 atgcaccgttgatgggggt.....aacagaaaggacacctctc 861

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_16Dec04:*

1: Geneseqn1980s:*

2: Geneseqn1990s:*

3: Geneseqn2000s:*

4: Geneseqn2001as:*

5: Geneseqn2001bs:*

6: Geneseqn2002as:*

7: Geneseqn2002bs:*

8: Geneseqn2003as:*

9: Geneseqn2003bs:*

10: Geneseqn2003cs:*

11: Geneseqn2003ds:*

12: Geneseqn2004as:*

13: Geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	861	100.0	864	11	Adn38809 Cancer/an
2	861	100.0	1321	6	Abk12137 Human cdn
3	861	100.0	4839	8	Acc49552 Tumour-as
4	861	100.0	4839	11	Adp65809 Human STA
5	861	100.0	4839	11	Adp65729 Human tra
6	861	100.0	4839	12	Adm67045 Human hom
7	861	100.0	4839	13	Adr65875 Human pro
8	861	100.0	4839	13	Adr66778 Human pro
9	861	100.0	4911	13	Acn40804 Tumour-as
10	859.4	99.8	1383	10	Adc37326 Nuclear f
11	755.2	87.7	969	3	Aaa75151 cDNA enco
12	754.2	87.6	1140	6	Abk92120 Prostate
13	754.2	87.6	1141	10	Adb75588 Prostate
14	754.2	87.6	1850	8	Acc49536 Tumour-as
15	754.2	87.6	4527	11	Adl83313 Human and
16	753.6	87.5	969	3	Aaa75164 cDNA clon
17	753.6	87.5	969	3	Aaa75163 cDNA clon
18	753.6	87.5	969	3	Aaa75165 cDNA clon
19	753.6	87.5	1140	10	Ada60105 Human and
20	753.6	87.5	1140	10	Adh62276 Human PME

21	753.6	87.5	1140	12	ADO39826
22	752.8	87.4	759	10	ADFI7545
23	752.8	87.4	759	10	ADH62277
24	752.8	87.4	759	12	ADO39827
25	752.6	87.4	806	8	ACC49537
26	752.6	87.4	1061	3	AAA47429
27	752.6	87.4	1085	10	ADC37324
28	752.6	87.4	1334	8	ABZ36103
29	742.4	86.2	1066	4	AAI57868
30	712	82.7	1069	4	AAI59654
31	612.4	71.1	878	6	ABK12142
32	544.4	63.2	1583	6	ABS61424
33	462.2	53.7	1713	3	AAA75152
34	460.6	53.5	1713	3	AAA75167
35	460.6	53.5	1713	3	AAA75166
36	445.6	51.8	693	6	ABK12143
37	445.6	51.8	693	6	ABK12143
38	417.4	48.5	812	2	AAZ52964
39	417	48.4	474	10	ABZ84732
40	401.4	46.6	408	5	AAE65983
41	400.6	46.5	673	6	ABT09178
42	400.6	46.5	673	12	ADG45576
43	400.6	46.5	673	12	ADH22874
44	352.2	40.9	8018	11	ACN44959
45	352.2	40.9	8494	5	AAS77304

ALIGNMENTS

RESULT 1

ADN38809

ID ADN38809 standard; cDNA; 864 BP.

XX

AC ADN38809;

XX

DT 17-JUN-2004 (first entry)

XX

DE Cancer/angiogenesis/fibrosis-related nucleic acid, SEQ ID NO:127.

XX

KW Human; differential expression; cancer; angiogenic disorder;

KW fibrotic disorder; psoriasis; ischaemia; heart disease; atherosclerosis;

KW inflammatory disease; autoimmune disease;

KW retinal neovascularisation syndrome; scarring; uterine fibroid;

KW detection; diagnosis; prognosis; drug screening; drug targeting;

KW wound healing; contraception; cytostatic; cardiant; immunomodulatory;

KW vulnery; gene therapy; vaccine; gene; ss.

XX

OS Homo sapiens.

XX

PN WO2003042661-A2.

XX

PD 22-MAY-2003.

XX

PF 13-NOV-2002; 2002WO-US036810.

XX

PR 13-NOV-2001; 2001US-0350666P.

XX

PR 21-NOV-2001; 2001US-0332464P.

XX

PR 29-NOV-2001; 2001US-0334393P.

XX

PR 03-DEC-2001; 2001US-0335394P.

XX

PR 14-DEC-2001; 2001US-0340376P.

XX

PR 08-JAN-2002; 2002US-0347211P.

XX

PR 10-JAN-2002; 2002US-0347349P.

XX

PR 08-FEB-2002; 2002US-0355250P.

XX

PR 13-FEB-2002; 2002US-0356714P.

XX

PR 20-FEB-2002; 2002US-0359077P.

XX

PR 29-MAR-2002; 2002US-0368809P.

XX

PR 04-APR-2002; 2002US-0370110P.

XX

PR 12-APR-2002; 2002US-0372246P.

XX

PR 05-JUN-2002; 2002US-0386614P.

XX

PR 16-JUL-2002; 2002US-0396839P.

XX

PR 22-JUL-2002; 2002US-0397775P.

XX

PR 22-JUL-2002; 2002US-0397845P.

XX

[illegible]

Db	1133	GGGTCTCTCTTCAGCAGCAGCAGCAGCAGTGGCGCCGCCCTCTTGTCTGGAGGGACCCGG	1199			
Qy	781	CTCCACCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAAGAT	840			
Db	1193	CTCCACCCACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCAAGAGAAGAT	1252			
Qy	841	AAACAGAAAGGACACCTCTC	861			
Db	1253	AAACAGAAAGGACACCTCTC	1273			
RESULT 3						
ACC49552						
ID	ACC49552 standard; cDNA; 4839 BP.					
XX	XX					
XX	ACC49552;					
XX	XX					
DT	01-JUL-2003 (first entry)					
XX	XX					
DE	Tumour-associated antigenic target protein TAT379 SEQ ID NO:119.					
XX	XX					
KW	Human; tumour-associated antigenic target; TAT; tumour; diagnosis;					
KW	cancer; gene; ss.					
XX	XX					
OS	Homo sapiens.					
XX	XX					
PN	WO2003024392-A2.					
XX	XX					
PD	27-MAR-2003.					
XX	XX					
PF	11-SEP-2002; 2002WO-US028859.					
XX	XX					
PR	18-SEP-2001; 2001US-0323268P.					
PR	19-OCT-2001; 2001US-0339227P.					
PR	07-NOV-2001; 2001US-0336827P.					
PR	20-NOV-2001; 2001US-0331906P.					
PR	02-JAN-2002; 2002US-0345444P.					
PR	03-APR-2002; 2002US-0369724P.					
PR	19-AUG-2002; 2002US-0404809P.					
XX	XX					
PA	(GETH) GENENTECH INC.					
XX	XX					
PI	Frantz G, Hillan KJ, Phillips HS, Polakis P, Spencer SD;					
PI	Williams PM, Wu TD, Zhang Z;					
XX	XX					
DR	WPI; 2003-354551/33.					
DR	P-PSDB; ABP97234.					
XX	XX					
PT	New antibodies against tumor-associated antigenic target polypeptide,					
PT	useful for treating or diagnosing tumors or cancers in mammals, e.g.					
PT	prostate cancer, lung cancer, prostate adenocarcinomas or renal cell					
PT	carcinomas.					
XX	XX					
PS	Claim 2; Fig 119; 285pp; English.					
XX	XX					
CC	ACC49493 to ACC49552 encode the human tumour-associated antigenic target					
CC	(TAT) proteins given in ABP97175 to ABP97234. The present invention					
CC	describes an isolated antibody that binds to a polypeptide having at					
CC	least 80 % sequence identity to any of the 60 150-800 residue amino acid					
CC	sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking					
CC	its associated signal peptide, encoded by any of the 60 2000-3000 base					
CC	pair sequences (S2), given in ACC49493 to ACC49552. TAT proteins have					
CC	cytostatic activity. The antibody can be used for treating or diagnosing					
CC	tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast					
CC	cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal					
CC	cell carcinomas, or thyroid cancer					
XX	XX					
SQ	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;					
Query Match 100.0%; Score 861; DB 8; Length 4839;						
Best Local Similarity 100.0%; Pred. No. 2.9e-167;						
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						

PA (MILL-) MILLENNIUM PHARM INC.
XX Barnes TM, Holtzman DA, Sharp JD, Fraser CC;
XX WPI; 2000-579269/54.
XX P-PSDB; AAB18449.
XX Novel human and murine secreted proteins designated TANGO 216, 261, 262,
XX 266 and 267 useful as modulating agents of cellular processes, e.g. for
XX treating cancer.
XX Claim 2; Fig 5; 175pp; English.
XX The present sequence encodes a human TANGO 261 polypeptide. The
XX specification also describes TANGO 266, TANGO 216, TANGO 262, and TANGO
XX 267. The TANGO polypeptides can be used to modulate cellular
XX proliferation, modulate cellular differentiation and/or modulate cellular
XX adhesion. The proteins can be used to treat any von Willebrand factor-
XX associated disorder, regulate extracellular matrix structuring, cellular
XX adhesion, and cell trafficking and/or migration, modulate cellular
XX interactions, modulate cell adhesion in proliferative disorders, such as
XX cancer, modulate the proliferation, differentiation, and/or function of
XX cells that appear in the bone marrow, and leukocytes, treat bone marrow,
XX blood and hematopoietic associated diseases and disorders, atelectasis,
XX pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial
XX asthma and bronchiectasis, intestinal disorders, spleen associated
XX diseases, modulate renal disorders, treat cardiovascular disorders such
XX as ischemic heart disease, modulate the proliferation, differentiation,
XX and/or function of bone and cartilage cells and to treat bone and/or
XX cartilage associated diseases or disorder. They may also be used to treat
XX disorders associated with the ovaries, cerebral oedema, hydrocephalus,
XX brain herniations, iatrogenic disease, inflammations, bacterial and viral
XX meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's
XX disease, multiple sclerosis, brain cancers, hydrocephalus and
XX encephalitis, and treat hepatic disorders
XX
XX Sequence 969 BP; 211 A; 316 C; 294 G; 148 T; 0 U; 0 Other;
XX
XX Query Match 87.7%; Score 755.2; DB 3; Length 969;
XX Best Local Similarity 99.6%; Pred. No. 1.3e-145;
XX Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 102 GGAGATACGGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGTGAT 161
XX 2 GGAGATGGCGAGCTGGAGTTTGTTCAGATCATCATCTGCTGGTGTGATGTGAT 61
XX
XX 162 GGTGGTGGTATCATCGTCTGCTGAGCCACTACAGTCTGTCAGGTCCTTCATCAG 221
XX 62 GGTGGTGGTATCATCGTCTGCTGAGCCACTACAGTCTGTCAGGTCCTTCATCAG 121
XX
XX 222 CCGGCACAGCCAGGGCGGAGGAGAGATGCCCTGCTCAGAGGATGCCCTGTGGCC 281
XX 122 CCGGCACAGCCAGGGCGGAGGAGAGATGCCCTGCTCAGAGGATGCCCTGTGGCC 181
XX
XX 282 CTGCGAGAGCACAGTGTTCAGGCAACGGAATCCAGAGCCGCAAGTCTACGCCCGGCTCG 341
XX 182 CTGCGAGAGCACAGTGTTCAGGCAACGGAATCCAGAGCCGCAAGTCTACGCCCGGCTCG 241
XX
XX 342 GCCCAGCGAGCCGCTGGCGGTGGCGCCCTTCGCCAGCGGGAGGCTTCACCGCTTCCA 401
XX 242 GCCCAGCGAGCCGCTGGCGGTGGCGCCCTTCGCCAGCGGGAGGCTTCACCGCTTCCA 301
XX
XX 402 GCCCAGCTATTCCTGCTGAGCAGCAGAGATCGACCTGCCACCCACCATCTCGCTGTGAGA 461
XX 302 GCCCAGCTATTCCTGCTGAGCAGCAGAGATCGACCTGCCACCCACCATCTCGCTGTGAGA 361
XX
XX 462 CGGGAGGAGCCGCCACCTTACAGGGCCCTGCAACCTTCAGCTTCGGGACCCCGAGCA 521
XX 362 CGGGAGGAGCCGCCACCTTACAGGGCCCTGCAACCTTCAGCTTCGGGACCCCGAGCA 421
XX
XX 522 GCAGCTGGAATCAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCACAG 581
XX 422 GCAGCTGGAATCAACCGGAGTGGTGGCGGACCCCAACAGAACCATCTTCACAG 481

QY 582 TGACCTGATGGATAGTCCAGGGCTGGCGGGCCCTGCCCCCCCCCAGCAGTAACCTCGGCAT 641
DB 482 TGACCTGATGGATAGTCCAGGGCTGGCGGGCCCTGCCCCCCCCCAGCAGTAACCTCGGCAT 541
QY 642 CAGCGCCAGTGTCTACGGCAGCGGGCGGCATGGAGGGGGCCGCCGCCACCTACACGCA 701
DB 542 CAGCGCCAGTGTCTACGGCAGCGGGCGGCATGGAGGGGGCCGCCGCCACCTACACGCA 601
QY 702 GGTTCATCGGCACCTACCCCGGGGTCTCTCTTCCAGCACCAGCAGAGCGTGGCGGCCCTC 761
DB 602 GGTTCATCGGCACCTACCCCGGGGTCTCTCTTCCAGCACCAGCAGAGCGTGGCGGCCCTC 661
QY 762 CTTGCTGGAGGGAGCCCGGCTCCACACACACACATCGCGGCCCTTAGAGAGCGCAGCAT 821
DB 662 CTTGCTGGAGGGAGCCCGGCTCCACACACACATCGCGGCCCTTAGAGAGCGCAGCAT 721
QY 822 CTGCGACCAAGAGCAAGGATATAAAGAGAAAGGACACCTCTC 861
DB 722 CTGCGACCAAGAGCAAGGATATAAAGAGAAAGGACACCTCTC 761

RESULT 12
ABK92120
ID ABK92120 standard; DNA; 1140 BP.
XX
XX AC ABK92120;
XX DT 15-AUG-2002 (first entry)
XX DE Prostate cancer-associated DNA sequence #6.
XX KW Prostate cancer; prostate tumour tissue; human; mammal; cytostatic;
XX KM gene therapy; gene; ds.
XX OS Mammalia.
XX PN WO200230268-A2.
XX PD 18-APR-2002.
XX PF 12-OCT-2001; 2001WO-US032045.
XX PR 13-OCT-2000; 2000US-00687576.
XX PR 08-DEC-2000; 2000US-00733288.
XX PR 08-DEC-2000; 2000US-00733742.
XX PR 24-JAN-2001; 2001US-0263957P.
XX PR 16-MAR-2001; 2001US-0276791P.
XX PR 16-MAR-2001; 2001US-0276888P.
XX PR 06-APR-2001; 2001US-0281922P.
XX PR 24-APR-2001; 2001US-0286214P.
XX PR 30-APR-2001; 2001US-00847046.
XX PR 04-MAY-2001; 2001US-0288589P.
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX Gish KC, Mack DH, Wilson KE, Afar D, Hevezi P;
XX WPI; 2002-471335/50.
XX P-PSDB; ABG61805.
XX
XX Detecting a prostate cancer-associated transcript in a cell in a patient,
XX useful for diagnosing prostate cancer (PC) or screening modulators of PC,
XX by determining if prostate cancer-associated genes are expressed in a
XX prostate tissue.
XX
XX Claim 22; Page 305; 436pp; English.
XX
XX The present invention relates to methods of detecting a prostate cancer-
XX associated transcript in a cell from a patient. The method comprises
XX contacting a biological sample from the patient with prostate cancer-
XX associated polynucleotides (designated PC genes) that selectively
XX hybridise to a sequence that is at least 80% identical to them. The

CC prostate cancer-associated polynucleotide sequences are differentially
CC expressed in prostate tumour tissue or in prostate cancer and are derived
CC from the tissues of various organisms such as humans or other mammals
CC (e.g. mice, sheep and dogs). The methods of the invention are useful for
CC diagnosing and treating prostate cancer in mammals. The prostate cancer-
CC associated genes are useful for diagnosing or treating prostate cancer,
CC as well as for identifying modulators of prostate cancer or agents that
CC inhibit prostate cancer. The nucleic acid sequences are particularly
CC useful in gene therapy, as a vaccine or in antisense applications.
CC ABK92115-ABK92263 represent prostate cancer-associated polynucleotide
CC sequences
XX

SQ Sequence 1140 BP; 270 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match 87.6%; Score 754.2; DB 6; Length 1140;
Best Local Similarity 98.3%; Pred. No. 2.1e-145;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTTGTTCCAGAGCAGTGGAGTACGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 146
DB 77 TCTCCTCGAAACCCAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136
QY 147 GGTGATGATGGTGTGTTGTGATCAGTGTCTGCTGAGCCACTACAGCTGTCTGC 206
DB 137 GGTGATGATGGTGTGTTGTGATCAGTGTCTGCTGAGCCACTACAGCTGTCTGC 196
QY 207 ACGTCTCTTCATCAGCCGACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGA 266
DB 197 ACGTCTCTTCATCAGCCGACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGA 256
QY 267 AGATGCTGTGGCCCTTCGAGAGCACAGTGTTCAGGCAACCGAATCCAGAGCCGAGGT 326
DB 257 AGATGCTGTGGCCCTTCGAGAGCACAGTGTTCAGGCAACCGAATCCAGAGCCGAGGT 316
QY 327 CTAGCCGCCGCTCGGCCACCGACCGCTGGCGGTGCGCCCTTGGCCAGCGGAGCG 386
DB 317 CTAGCCGCCGCTCGGCCACCGACCGCTGGCGGTGCGCCCTTGGCCAGCGGAGCG 376
QY 387 CTTCACCGCTTCAGGCCACCTATCGTACCTGACGACGAGATCGACCTGCCACCCAC 446
DB 377 CTTCACCGCTTCAGGCCACCTATCGTACCTGACGACGAGATCGACCTGCCACCCAC 436
QY 447 CATCTGCTGTACAGCGGAGAGCCGCCACCTTACAGGGCCCTGACCTCCAGCT 506
DB 437 CATCTGCTGTACAGCGGAGAGCCGCCACCTTACAGGGCCCTGACCTCCAGCT 496
QY 507 TCGGGACCCGAGCAGCTGGAACCTGACCGGGAGTGGTGGCGCACCCCAACAG 566
DB 497 TCGGGACCCGAGCAGCTGGAACCTGACCGGGAGTGGTGGCGCACCCCAACAG 556
QY 567 AACCATCTTCAGCAGTGACCTGATGATGTCAGGCTGGGGCGGCCCTTGGCCGCCAG 626
DB 557 AACCATCTTCAGCAGTGACCTGATGATGTCAGGCTGGGGCGGCCCTTGGCCGCCAG 616
QY 627 CAGTAATCGGGATACGCCCACTGCTGTAACGAGCGGGCGGCGATGAGGGCGGCC 686
DB 617 CAGTAATCGGGATACGCCCACTGCTGTAACGAGCGGGCGGCGATGAGGGCGGCC 676
QY 687 GCCCACTACAGGAGTCAATCGCCCACTACCGGGGTCTCTTCCAGCACCCAGAG 746
DB 677 GCCCACTACAGGAGTCAATCGCCCACTACCGGGGTCTCTTCCAGCACCCAGAG 736
QY 747 CAGTGGGCGGCCCTCTTGTGAGGGGACCCGGCTCCACACACACATCGCGCCCT 806
DB 737 CAGTGGGCGGCCCTCTTGTGAGGGGACCCGGCTCCACACACACATCGCGCCCT 796
QY 807 AGAGCGGCGGCCCTCTGAGGCAAGAGAGGATTAACGAAAGGACACCCCTCTC 861
DB 797 AGAGCGGCGGCCCTCTGAGGCAAGAGAGGATTAACGAAAGGACACCCCTCTC 851

RESULT 13
ADB75588

ID ADB75588 standard; cDNA; 1141 BP.

AC ADB75588;

DT 04-DEC-2003 (first entry)

DE Prostate cancer marker cDNA.

KW Prostate; cancer; cytostatic; gene therapy; marker; ss.

OS Homo sapiens.

PN WO2003009814-A2.

PD 06-FEB-2003.

PF 25-JUL-2002; 2002WO-US023913.

PR 25-JUL-2001; 2001US-0307982P.

PR 22-AUG-2001; 2001US-0314356P.

PR 25-SEP-2001; 2001US-0325020P.

PR 12-DEC-2001; 2001US-0341746P.

PR 05-MAR-2002; 2002US-0362158P.

XX (MILL-) MILLENNIUM PHARM INC.

XX Schlegel R, Monahan JE, Endege WO, Gannavarapu M, Gorbacheva B;

PI Hoern S, Kamakar S, Wonsley AM, Giatt K, Zhao X, Anderson D;

DR WPI; 2003-248033/24.

XX New nucleic acid molecule, useful for diagnosing or treating prostate

PT cancer.

XX Disclosure; SEQ ID NO 412; 99pp; English.

XX The invention relates to newly discovered cancer markers associated with

CC the cancerous state of prostate cells. Also disclosed is a method of

CC assessing whether a patient is afflicted with prostate cancer. The method

CC of the invention involves assessing whether a patient is afflicted with

CC prostate cancer by comparing the level of expression of a marker in a

CC patient sample and the normal level of expression of the marker in a

CC control non-prostate cancer sample, where a significant increase in the

CC level of expression of the marker in the patient sample and the normal

CC level indicates that the patient is afflicted with prostate cancer.

CC Nucleic acids of the invention are useful for diagnosing or treating

CC prostate cancer, and may be useful in gene therapy. Sequences given in

CC ADB75177-ADB75631 represent marker cDNA and proteins. Note: The sequence

CC data for this patent did not form part of the printed specification, but

CC was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences.

XX

SQ Sequence 1141 BP; 271 A; 350 C; 336 G; 184 T; 0 U; 0 Other;

Query Match 87.6%; Score 754.2; DB 10; Length 1141;

Best Local Similarity 98.3%; Pred. No. 2.1e-145;

Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTTGTTCCAGAGCAGTGGAGTACGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 146

DB 77 TCTCCTCGAAACCCAGGCAATGGCGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136

QY 147 GGTGATGATGGTGTGTTGTGATCAGTGTCTGCTGAGCCACTACAGCTGTCTGC 206

DB 137 GGTGATGATGGTGTGTTGTGATCAGTGTCTGCTGAGCCACTACAGCTGTCTGC 196

QY 207 ACGTCTCTTCATCAGCCGACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGA 266

DB 197 ACGTCTCTTCATCAGCCGACAGCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGA 256

QY 267 AGATGCTGTGGCCCTTCGAGAGCACAGTGTTCAGGCAACCGAATCCAGAGCCGAGGT 326

DB 257 AGATGCTGTGGCCCTTCGAGAGCACAGTGTTCAGGCAACCGAATCCAGAGCCGAGGT 316

QY 327 CTAGCCCGCTCGGCCACCGACCGCTGGCGCTGCGCCCTTCGCCAGCGGAGCG 386
DB 317 CTAGCCCGCTCGGCCACCGACCGCTGGCGCTGCGCCCTTCGCCAGCGGAGCG 376
QY 387 CTTCCACCGCTTCAGCGCCACCTATCGTACCTGTCAGCAGAGATCGACCTGCCACCCAC 446
DB 377 CTTCCACCGCTTCAGCGCCACCTATCGTACCTGTCAGCAGAGATCGACCTGCCACCCAC 436
QY 447 CATCTCGCTGTACAGCGGGAGGAGCCCAACCTACCGGGCCCTTCGACCTCCAGCT 506
DB 437 CATCTCGCTGTACAGCGGGAGGAGCCCAACCTACCGGGCCCTTCGACCTCCAGCT 496
QY 507 TCGGACCCCGAGCAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGCAGCCCAACAG 566
DB 497 TCGGACCCCGAGCAGCAGCTGGAACCTGAACCGGGAGTGGTGGCGCAGCCCAACAG 556
QY 567 AACCATCTTCGACAGTCACTGATGATAGTGCAGGCTGGGGCCCTGCCCCCAG 626
DB 557 AACCATCTTCGACAGTCACTGATGATAGTGCAGGCTGGGGCCCTGCCCCCAG 616
QY 627 CAGTAATCTCGGGCATCAGCGCCACGTCGTACGGCAGCGGGCGGCGCATGGAGGGCGCGCC 686
DB 617 CAGTAATCTCGGGCATCAGCGCCACGTCGTACGGCAGCGGGCGGCGCATGGAGGGCGCGCC 676
QY 687 GCCCACCCTACAGCAGAGTCACTCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGAG 746
DB 677 GCCCACCCTACAGCAGAGTCACTCGGCCACTACCCGGGGTCTCTTCCAGCACCAGCAGAG 736
QY 747 CAGTGGCGCGCTCTCTTGGGGGAGCCCGGCTCCACACACACACATCGGGCCCT 806
DB 737 CAGTGGCGCGCTCTCTTGGGGGAGCCCGGCTCCACACACACACATCGGGCCCT 796
QY 807 AGAGAGCGCGCATCTCGGAGCAAGAGAGAGATTAACAGAGGATTAACAGAGGACACCTCTC 861
DB 797 AGAGAGCGCGCATCTCGGAGCAAGAGAGAGATTAACAGAGGATTAACAGAGGACACCTCTC 851

RESULT 14

ID ACC49536 standard; cDNA; 1850 BP.

AC ACC49536;

XX 01-JUL-2003 (first entry)

XX Tumour-associated antigenic target protein TAT180 cDNA SEQ ID NO:44.

XX Human; tumour-associated antigenic target; TAT; tumour; diagnosis;
KW cancer; gene; ss.

XX Homo sapiens.

XX W0203024392-A2.

XX 27-MAR-2003.

XX 11-SEP-2002; 2002W0-US028859.

XX 18-SEP-2001; 2001US-0323268P.

XX 19-OCT-2001; 2001US-0339227P.

XX 07-NOV-2001; 2001US-0336827P.

XX 20-NOV-2001; 2001US-0331906P.

XX 02-JAN-2002; 2002US-0345444P.

XX 03-APR-2002; 2002US-0369724P.

XX 19-AUG-2002; 2002US-0404809P.

XX (GETH) GENENTECH INC.

XX Frantz G. Hillan KJ, Phillips HS, Polakis P, Spencer SD;

XX Williams PM, Wu TD, Zhang Z;

XX WPI; 2003-354551/33.

DR P-PSDB; ABP97218.

XX New antibodies against tumor-associated antigenic target polypeptide,
PT useful for treating or diagnosing tumors or cancers in mammals, e.g.
PT prostate cancer, lung cancer, prostate adenocarcinomas or renal cell
PT carcinomas.

XX Claim 2; Fig 44; 285pp; English.

XX ACC49493 to ACC4952 encode the human tumour-associated antigenic target
CC (TAT) proteins given in ABP97175 to ABP97234. The present invention
CC describes an isolated antibody that binds to a polypeptide having at
CC least 80 % sequence identity to any of the 60 150-800 residue amino acid
CC sequences (S1), given in ABP97175 to ABP97234, comprising (S1), lacking
CC its associated signal peptide, encoded by any of the 60 2000-3000 base
CC pair sequences (S2), given in ACC49493 to ACC4952. TAT proteins have
CC cytostatic activity. The antibody can be used for treating or diagnosing
CC tumours or cancers in mammals, e.g. prostate cancer, lung cancer, breast
CC cancer, colon cancer, ovarian cancer, prostate adenocarcinomas, renal
CC cell carcinomas, or thyroid cancer

XX SQ Sequence 1850 BP; 477 A; 472 C; 498 G; 403 T; 0 U; 0 Other;

Query Match 87.6%; Score 754.2; DB 8; Length 1850;

Best Local Similarity 98.3%; Pred. No. 2.2e-145;

Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTTGTTCCAGAGCATGGAGATCACGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 146

DB 77 TCTCTCGGAAACAGGCATGGGAGCTGGAGTTTGTTCAGATCATCATCGTGGT 136

QY 147 GGTGATGATGTTGATGTTGTTGATACGTGCTGTGAGCCACTTACAGTGTCTGC 206

DB 137 GGTGATGATGTTGATGTTGTTGATACGTGCTGTGAGCCACTTACAGTGTCTGC 196

QY 207 ACGTCTTTCATCAGCGGCGCACAGCGGGCGGAGAGAGATGCTCTCTCAGA 266

DB 197 ACGTCTTTCATCAGCGGCGCACAGCGGGCGGAGAGAGATGCTCTCTCAGA 256

QY 267 AGGATGCTGTGGCCCTCGGAGAGCAGTGTTCAGGCAACGGAATCCAGAGCGCAGGT 326

DB 257 AGGATGCTGTGGCCCTCGGAGAGCAGTGTTCAGGCAACGGAATCCAGAGCGCAGGT 316

QY 327 CTAGCGCCCGCTCGGCCACACCGCGCTGGCGCTGCGCCCTTCGCCAGCGGAGCG 386

DB 317 CTAGCGCCCGCTCGGCCACACCGCGCTGGCGCTGCGCCCTTCGCCAGCGGAGCG 376

QY 387 CTTCCACCGCTTCAGCGCCACCTATCGTACCTGCGAGCAGATCGACTGCCACCCAC 446

DB 377 CTTCCACCGCTTCAGCGCCACCTATCGTACCTGCGAGCAGATCGACTGCCACCCAC 436

QY 447 CATCTCGCTGTACAGCGGGAGGAGCCCAACCTTACCGGGCCCTTCGACCTCCAGCT 506

DB 437 CATCTCGCTGTACAGCGGGAGGAGCCCAACCTTACCGGGCCCTTCGACCTCCAGCT 496

QY 507 TCGGGAACCCCGAGCAGCAGCTGGAACTGAAACCGGGAGTGGTGGCGCACCCCCAAACAG 566

DB 497 TCGGGAACCCCGAGCAGCAGCTGGAACTGAAACCGGGAGTGGTGGCGCACCCCCAAACAG 556

QY 567 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 626

DB 557 AACCATCTTCGACAGTGAACCTGATGATGATGATGATGATGATGATGATGATGATGAT 616

QY 627 CAGTAATCTCGGGCATCAGCGCCACGTCGTACGGCAGCGGGCGGCGCATGGAGGGCGGCC 686

DB 617 CAGTAATCTCGGGCATCAGCGCCACGTCGTACGGCAGCGGGCGGCGCATGGAGGGCGGCC 676

QY 687 GCCCACCCTACAGCAGAGTCACTCGGCCACCTACCGGGGTCTCTTCCAGCACCAGCAGAG 746

DB 677 GCCCACCCTACAGCAGAGTCACTCGGCCACCTACCGGGGTCTCTTCCAGCACCAGCAGAG 736

QY 747 CAGTGGCGCGCTCTCTTGGTGGAGGGGACCCGGCTCCACACACACATCGGGCCCT 806

Search completed: February 19, 2005, 11:44:06
Job time : 462.884 secs

SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 921 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1...921
OTHER INFORMATION: Clone 22 coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-091-952A-7

Query Match 40.9%; Score 352.2; DB 3; Length 921;
Best Local Similarity 73.1%; Pred. No. 1.2e-71;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 94 CAGAGCATGAGATCAGCGAGCTGGAGTTGTCAGATCATCATCATCGTGGTGGTATG 153
DB 166 CCGGGCATCTTCACTCGAGCTGGAGTTGCCCAATCATCATCATCGTGGTGGTGC 225
QY 154 ATGTTGATGTTGGTGGTATCAGTCTGCTGAGCCACTACAGCTGTGACCGTCC 213
DB 226 ACGTGTGATGTTGGTGGTATCAGTCTGCTGCTGAACCACTACAAATCTCACCGGTCC 285
QY 214 TTCTATCAGCCGCGCACACCGAGCGCGGAGGAGAGATGCCCTGTCTCTCAGAAGATGC 273
DB 286 TTCTATCAACCGCCGACACAGCGCGGAGGAGCGGCTGCCGAGGAGGTGC 345
QY 274 CTGTGGCCCTCGAGAGACACAGTGTCTAGGCAACGGAATCCAGAGCGCGAGGTCTAGCC 333
DB 346 CTGTGGCCCTTCAGACAGCGCGCACCGCGGTGGG-----CGCCTCGAGATCATGCAT 399
QY 334 CCGCTCGGCCACCGACCGCTGGCGTCCGCGCTTCGCCCGGAGCGGCGCTTCCAC 393
DB 400 GCGCCGCGGTCCAGGAGACAGGTTACAGCGCGCTTCCTTCATCAGAGGATCGCTTCAGC 459
QY 394 CGCTTCAGGCCACCTATCGTACTCTGACGACGAGATGACCTGCCACCCACCATCTCG 453
DB 460 CGCTTCAGGCCACCTATCGTACTCTGACGACGAGATGATCTCTCTCCACCATCTCC 519
QY 454 CTGTTCAGCGGGAGGAGCGGCCACCTACAGGGCCCTTCGACCTCTCAGCTTCGGGAC 513
DB 520 CTGTTCAGCGGTGAAGAGCGCACCTCTTACAGGGGCGCTTCACCTGTGACGTCCGGGAC 579
QY 514 CCGGAGCGGAGCTGGAACTGAACCGGAGTTCGGTGGCGGACCCCAACAGACCATC 573
DB 580 CCGTGAACAGAGATGGAACTCAACCGGAGTTCGGTGGAGCGGCCCAACCGAACCAT 639
QY 574 TTGCAGAGTACCTGATGGATAGTGGCAGG---CTGGGCGGCCCTCTGCCCGCCCGAGT 630
DB 640 TTTCAGAGTGAATTAATAGACATTCCTATGTATAGCGGGGGTTCATGATCCACCGAGC 699
QY 631 AACTCGGGCATCAGCGCCACGTGCTACGGAGCGCGGCGGCGATGGAGGGGCGCGCGCC 690

DB 700 AACTCGGGCATCAGTCAAGCACCTGCAGCAGTAAACGGGAGGATGGAGGGGCCACCCCCC 759
QY 691 ACCTCAGCGAGGTCTATCGGCCACTACCCGGGGTCTCTTCCAGCACCGAGCAGAGCAG 749
DB 760 ACATCAGCGAGGTGATGGGCCACCCAGCGGCGCTCTTCTCTCCATCATCAGCGCAG 818
RESULT 4
US-09-091-952A-6
Sequence 6, Application US/09091952A
Patent No. 6458532
GENERAL INFORMATION:
APPLICANT: Detera-Wadleigh, Sevilla D.
Gershon, Elliot S.
Badner, Judith A.
Goldin, Lynn R.
Berrettini, Wade H.
Yoshikawa, Takeo
Sanders, Alan R.
Esterling, Lisa E.
TITLE OF INVENTION: Chromosomal Markers and Diagnostic
Tests for Manic-Depressive Illness
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8065 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: -
LOCATION: 1...8065
OTHER INFORMATION: Clone 22
FEATURE:
NAME/KEY: CDS
LOCATION: 116...1036
OTHER INFORMATION: Clone 22 coding region
FEATURE:
NAME/KEY: misc feature
LOCATION: 452...505
OTHER INFORMATION: alternatively spliced portion


```
; NAME/KEY: misc feature
; LOCATION: 5595...5685
; OTHER INFORMATION: amplified region for genotyping
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-091-952A-6

Query Match      40.9%; Score 352.2; DB 3; Length 8065;
Best Local Similarity 73.1%; Pred. No. 2.2e-71;
Matches 482; Conservative 0; Mismatches 168; Indels 9; Gaps 2;

QY 94 CAGAGCATGGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTGCTGGTGGTATG 153
Db 281 CCGGCGATCTTCAACTCGGAGCTGGAGTTGCCCAAAATCATCATCTGCTGGTGGT 340
QY 154 ATGTGTATGGTGGTGGTATCATCTGCTGGAGCACTACAAAGCTGTCTGCAAGTCC 213
Db 341 ACGGTATGGTGGTGGTATCTGCTGCTGCTGCAACCACTACAAAGTCTTCAACGGTCC 400
QY 214 TTCTATCGCCGGCAAGCAGCGGGCGGAGGAGAGATGCCCTGTCTCAGAGGATGC 273
Db 401 TTCTATCAACCCCGCAACAGAGCGGAGCGGAGGAGCGGCTGCCGAGGAGGAGTGC 460
QY 274 CTGTGGCCCTCGGAGAGACAGTGTCTAGGCNAACGGAATCCAGAGCGGAGGCTAGCC 333
Db 461 CTGTGGCCCTCAGACAGCGCGCGACCGCGGCTGGG-----CGCCTCGGAGATCATGCAT 514
QY 334 CCGCCTCGGCCCAACCGGAGCGGCTGGCGGCTGGCGGCTTTCGCCAGCGGAGCGCTTCCAC 393
Db 515 GCCCGCGGTCAGGAGACAGTTTACAGCGCGGCTTCTTCATCAGAGGAGTTCGTTTTCAGC 574
QY 394 CGCTTCCAGCCCACTATCGTACCTGAGCAAGATGCACTGAGTGCACCCCACTATCG 453
Db 575 CGCTTCCAGCCCACTATCGTACCTGAGCAAGATGCACTGAGTGCACCCCACTATCG 634
QY 454 CTGTTCAGACGGGAGGAGCGCCCACTTACAGGGCGGCTGACCTTCCAGCTTGGGAC 513
Db 635 CTGTTCAGACGGTGAAGAGCAGCTTCTTACAGGGCGGCTTCCAGCTTGGGAG 694
QY 514 CCGAGCAGCAGCTGGAACTGAACCGGGAGTTCGGTGGCGGCGGCGGCGGCGGCGGCGG 573
Db 695 CCTGAACAGCAGATGGAACCTCAACCGAGAGTTCGGTGGGCGGCGGCGGCGGCGGCGG 754
QY 574 TTGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 630
Db 755 TTGACAGTATTAATAGACATTTGATATGATAGCGGGGCTTCCATGATGATGATGATGAT 814
QY 631 AACTCGGGCATCAGCGCCACGTGTCTACGGCAGCGGGGCGGCGGCGGCGGCGGCGGCGG 690
Db 815 AACTCGGGCATCAGTGAACACCTGACGAGTAAACGGGAGGATGAGGGGCGGCGGCGGCGG 874
QY 691 ACTTACGAGGATGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 749
Db 875 ACATACGAGGATGATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 933
```

RESULT 5

```
US-09-311-021-65
; Sequence 65, Application US/09311021
; Patent No. 6706869
; GENERAL INFORMATION:
; APPLICANT: Wong, Gordon G.
; APPLICANT: Clark, Hilary
; APPLICANT: Fechtel, Kim
; APPLICANT: Agostino, Michael J.
; APPLICANT: Genetics Institute, Inc.
; TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; FILE REFERENCE: GI 6300-11A
; CURRENT APPLICATION NUMBER: US/09/311,021
; CURRENT FILING DATE: 1999-05-13
; NUMBER OF SEQ ID NOS: 268
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 65
; LENGTH: 937
```

```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-311-021-65

Query Match      40.8%; Score 351.6; DB 4; Length 937;
Best Local Similarity 73.0%; Pred. No. 1.7e-71;
Matches 482; Conservative 0; Mismatches 169; Indels 9; Gaps 2;

QY 93 CCAGAGCATGGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTGCTGGTGGTAT 152
Db 134 CTTGTCTTTAAAAAAGCGAGCTGGAGTTGCCCAAAATCATCATCTGCTGGTGGT 193
QY 153 GATGTGTATGGTGGTGGTATCATCTGCTGAGCCACTACAACTGCTGCTGCAAGTCC 212
Db 194 CACGGTATGGTGGTGGTATCATCTGCTGCTGTAACCACTACAAAGTCTTCCACCGGGT 253
QY 213 CTTTCATCAGCCGGCAACAGCCAGGCGGAGGAGAGAGATGCCCTGTCTCAGAAAGATG 272
Db 254 CTTTCATCAACCGCCGCAACAGAGCGGAGCGGAGGAGCGGCTGCCCGAGGAAGGGTG 313
QY 273 CTTGTGGCCCTCGGAGAGCAGATGTCAGGCAACGGAATCCAGAGCGGAGGCTTACGC 332
Db 314 CTTGTGGCCCTCAGACAGCGCGCGCACCGCGCTGGGG-----CGCCTCGGAGATCATGCA 367
QY 333 CCGCCTCGGCCCAACCGAGCGGCTGGCGGCTGGCGGCTTTCGCCAGCGGAGCGCTTCCA 392
Db 368 TGCCCGCGGTCAGGAGCAGGTTTACAGCGCGGCTTCTTCATCAGAGGAGTTCGTTTTCAG 427
QY 393 CCGCTTCCAGCCCACTATCTGCTGAGCAAGATGCACTGAGTGCACCTGCGGCGGCGGCGG 452
Db 428 CCGCTTCCAGCCCACTATCTGCTGAGCAAGATGCACTGAGTGCACCTGCGGCGGCGGCGG 487
QY 453 GCTGTTCAGACGGGAGGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 512
Db 488 CTTGTCCGAGCGGTGAAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 547
QY 513 CCGCAGCAGCAGCTGGAACTGAACCGGAGTTCGGTGGCGGCGGCGGCGGCGGCGGCGGCGG 572
Db 548 CCTGAACAGCAGATGGAACCTCAACCGAGAGTTCGGTGGGCGGCGGCGGCGGCGGCGGCGG 607
QY 573 CTTTCAGAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 629
Db 608 ATTGACAGTATTAATAGACATTTGCTATGATAGCGGGGCTTCCATGATGATGATGATGAT 667
QY 630 TAACTCGGGCATCAGCGCCACGTGTCTACGGCAGCGGCGGCGGCGGCGGCGGCGGCGGCGG 689
Db 668 CAACTCGGGCATCAGTGAACGACCTGACGAGTAAACGGGAGGATGAGGAGGCGGCGGCGGCGG 727
QY 690 CACCTACAGCGAGGTCATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 749
Db 728 CACATACAGCGAGTGTATGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 787
```

RESULT 6

```
US-09-091-952A-8
; Sequence 8, Application US/09091952A
; Patent No. 6458532
; GENERAL INFORMATION:
; APPLICANT: Detera-Wadleigh, Sevilla D.
; Gershon, Elliot S.
; Badner, Judith A.
; Goldin, Lynn R.
; Berrettini, Wade H.
; Yoshikawa, Takeo
; Sanders, Alan R.
; Esterling, Lisa E.
; TITLE OF INVENTION: Chromosomal Markers and Diagnostic Tests for Manic-Depressive Illness
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
```

STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PASCSEQ for Windows Version 2.0
CURRENT APPLICATION NUMBER: US/09/091,952A
FILING DATE: 19-Apr-1999
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/029,278
FILING DATE: 28-OCT-1996
APPLICATION NUMBER: PCT/US97/19381
FILING DATE: 28-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 015280-297100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX: <unknown>
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 867 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..867
OTHER INFORMATION: Clone 22 isoform 2 alternatively
spliced coding region
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-091-952A-8

Query Match 33.08; Score 284.2; DB 3; Length 867;
Best Local Similarity 68.71; Pred. No. 5e-56;
Matches 453; Conservative 0; Mismatches 143; Indels 63; Gaps 2;
QY 94 CAGAGATGGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCATCTGCTGGTGGTATG 153
DB 166 CCGGCACTTCACTCGGAGCTGGAGTTGCCCAATCATCATCTGCTGGTGGTGC 225
QY 154 ATGTTAGTGTGGTGTATCATGCTCTGCTGAGCCACTACAGTGTCTGCAAGTTC 213
DB 226 ACGTGTATGTTGGTGTCTATGCTGCTGCTGAACTACAAAGTCTCCACGCGTCC 285
QY 214 TTCTATGAGCGGCACACCGAGCGGAGGAGAGAGATGCCCTGTCTCAGAGGATGC 273
DB 286 TTCTATCAACCGCCCGAACCCAGAGCGGAGCGGAGGAGCGGCT----- 329
QY 274 CTGTGGCCCTCGGAGAGCACAGTGTCTAGGCAACGGAATCCAGAGCGGAGGCTACGCC 333
DB 330 -----GCCGAGATCATGTCAT 345
QY 334 CCGCCTCGGCCACCGACCGCTGGCGTGGCGCTTCGCCCGGAGCGGCTTCAC 393
DB 346 GCCCGGGTCCAGGAGACAGTTTCACAGCGCGTCTTCATCCAGAGGATGCTTCAGC 405
QY 394 CGCTTCAGGCCACCTATCGTACCTGTCAGACAGATGACCTGCCACCCACCATCTCG 453
DB 406 CGCTTCAGGCCACCTATCGTACCTGTCAGACAGATGATCTTCCTCCACCATCTCC 465
QY 454 CTGTTCAGCGGGAGGAGCCCGACCTTACAGGGCCCTGACCTCCAGCTTCGGGAC 513
DB 466 CTGTTCAGCGGTGAAGAGCACCTCTCTTACAGGGCCCTGACCTTCGAGCTCCGGGAC 525
QY 514 CCGAGCAGCAGCTGGAACTGAACCGGAGTCTGGTGGCGCACCCCGGCAACCAATC 573

DB 526 CCTGAACAGCAGATGGAACTCAACCGAGAGTTCGTGAGGGGCCCCACCAACCCGACCATTA 585
QY 574 TTGACAGTACCTGATGGATAGTCCAGG---CTGGGCGGCGCCCTGCCCCCCCCCAGCAGT 630
DB 586 TTTGACAGTATTTAATAGACATTGCTATGTATAGCGGGGTCCATGCCCCACCCAGCAGC 645
QY 631 AACTCGGGCATCAGCGCCACGTGCTACGGCAGCGGGCGCGCATGAGGGGCGCCGCCGCC 690
DB 646 AACTCGGGCATCAGTGCAGACCTGCAAGCACTGCAAGTAACCGGAGGATGAGGGGCGCCACCCGCC 705
QY 691 ACCTACAGCGAGTTCATCGGCCCACTACCGGGGTCTCTTCCAGACACCCAGCAGCAG 749
DB 706 ACATACAGCGAGGTGATGGGCCCAACCCAGGGCGCTCTTTCTCTCATCACCAGCGCAG 764
RESULT 7
US-09-621-976-2162
; Sequence 2162, Application US/09621976
; Patent No. 6639063
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Jobert, S.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.
; FILE REFERENCE: GENSET.054PR2
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT FILING DATE: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 2162
; LENGTH: 391
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 17..223
US-09-621-976-2162

Query Match 10.5%; Score 90.4; DB 4; Length 391;
Best Local Similarity 75.7%; Pred. No. 1.4e-11;
Matches 112; Conservative 0; Mismatches 36; Indels 0; Gaps 0;
QY 607 GGGCGCCCTGCCCCCCCCCAGCAGTAATCTCGGGCATCAGCGCCACGTGCTACGGCAGCGC 666
DB 26 GGGGGTCCATGCCACCCAGCAGCACTCGGGCATCAGTGCAGACCTTGCAGCAGTAAC 85
QY 667 GGGCGCATGAGGGGCGCGCCCACTACAGCAGGTCTATCGGCCACTACCCGGGTCC 726
DB 86 GGGAGGATGAGGGGCGCCACCCCCACATACAGCGAGGTGATGGGCCACCCAGCGCGCC 145
QY 727 TCCTTCCAGCACCCAGCAGCAGTGGGC 754
DB 146 TCTTCTCTCATCACCAGCGCAGAACGC 173

RESULT 8
US-09-902-540-6620
; Sequence 6620, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 6620


```

; PRIOR APPLICATION NUMBER: 09/183,175
; PRIOR FILING DATE: 1998-10-30
; PRIOR APPLICATION NUMBER: 09/223,094
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/223,546
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/224,246
; PRIOR FILING DATE: 1998-12-30
; PRIOR APPLICATION NUMBER: 09/259,388
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/122,458
; PRIOR FILING DATE: 1999-03-01
; PRIOR APPLICATION NUMBER: 09/312,359
; PRIOR FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: 09/336,536
; PRIOR FILING DATE: 1999-06-18
; PRIOR APPLICATION NUMBER: 09/342,687
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 09/345,464
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/365,164
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 09/399,723
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: 09/409,634
; PRIOR FILING DATE: 1999-09-30
; PRIOR APPLICATION NUMBER: 09/471,179
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 09/474,071
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/474,072
; PRIOR FILING DATE: 1999-12-29
; PRIOR APPLICATION NUMBER: 09/514,010
; PRIOR FILING DATE: 2000-02-25
; PRIOR APPLICATION NUMBER: 09/516,745
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/572,002
; PRIOR FILING DATE: 2000-05-14
; PRIOR APPLICATION NUMBER: 09/597,993
; PRIOR FILING DATE: 2000-06-19
; PRIOR APPLICATION NUMBER: 09/599,596
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 09/630,334
; PRIOR FILING DATE: 2000-07-31
; PRIOR APPLICATION NUMBER: 09/606,565
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/606,317
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: 09/665,666
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: 09/677,751
; PRIOR FILING DATE: 2000-09-30
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 55
; LENGTH: 969
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (6)...(761)
; US-09-796-753-55

Query Match      87.7%; Score 755.2; DB 10; Length 969;
Best Local Similarity 99.6%; Pred. No. 1.6e-191;
Matches 757; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 102 GGAGATCCGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGGTAT 161
Db 2 GGAGATGGCGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGGTGGTGGTGGTGGTAT 61

QY 162 GGTGGTGGTGGTATCAGCTGCTGCTGAGCCACTACAGCTGTTCGACGGTCTTTCATCAG 221
Db 62 GGTGGTGGTGGTATCAGCTGCTGCTGAGCCACTACAGCTGTTCGACGGTCTTTCATCAG 121

222 CCGGCAAGCAGCGGCGGAGGAGAGAAAGATGCGCTGTCTCTCAGAAAGATGCTGTGGCC 281
122 CCGGCAAGCAGCGGCGGAGGAGAGAAAGATGCGCTGTCTCTCAGAAAGATGCTGTGGCC 181
282 CTGGGAGAGCAGATGTCAGGCAACGGAATCCAGAGCGCGAGTCTTACGCGCGCTCG 341
182 CTGGGAGAGCAGATGTCAGGCAACGGAATCCAGAGCGCGAGTCTTACGCGCGCTCG 241
342 GCCCACCAGCGCTGCGCCCTTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 401
242 GCCCACCAGCGCTGCGCCCTTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 301
402 GCCCACCAGCGCTGCGCCCTTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 461
302 GCCCACCAGCGCTGCGCCCTTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCA 361
462 CGGGGAGGAGCGCGCCCTTACCGGCGCGCTTCCAGCGCGCTTCCAGCGCGCGGAGCA 521
362 CGGGGAGGAGCGCGCCCTTACCGGCGCGCTTCCAGCGCGCTTCCAGCGCGCGGAGCA 421
522 GCAGCTGGAACTGAAACCGGAGTGGTGGCGCGCAGCGCGCGCGCGCGCGCGCGCGAG 581
422 GCAGCTGGAACTGAAACCGGAGTGGTGGCGCGCAGCGCGCGCGCGCGCGCGCGAG 481
582 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 641
482 TGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 541
642 CAGCGCGAGTGTCTAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 701
542 CAGCGCGAGTGTCTAGCGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGAG 601
702 GGTGATCGGCGCTACCGCGGCTCTCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCTC 761
602 GGTGATCGGCGCTACCGCGGCTCTCTTCCAGCGCGCGCGCGCGCGCGCGCGCGCTC 661
762 CTTGCTGGAGGAGCGCGCGCTCCACACACACACACACACACACACACACACACACACAT 821
662 CTTGCTGGAGGAGCGCGCGCTCCACACACACACACACACACACACACACACACACAT 721
822 CTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 861
722 CTGGAGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 761

RESULT 10
US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarapu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Womsey, Angela M.
; APPLICANT: Glatt, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCES: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205,823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307,982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314,356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325,020
```


QY 627 CAGTAACTCGGGGATCAGCCGACGCTGCTAGCGGAGCGGGCGGCGCATGAGGGGCGGCC 686
DB 617 CAGTAACTCGGGGATCAGCCGACGCTGCTAGCGGAGCGGGCGGCGCATGAGGGGCGGCC 676
QY 687 GCCCACCCTACAGGAGGTCATCGGCCCACTACCCGGGGTCTCTCTCCAGCACCAGCAGAG 746
DB 677 GCCCACCCTACAGGAGGTCATCGGCCCACTACCCGGGGTCTCTCTCCAGCACCAGCAGAG 736
QY 747 CAGTGGGCGCCCTCTCTGCTGAGGGGACCCGGCTCCACACACACATCGGGCCCT 806
DB 737 CAGTGGGCGCCCTCTCTGCTGAGGGGACCCGGCTCCACACACACATCGGGCCCT 796
QY 807 AGAGGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 861
DB 797 AGAGGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 851

RESULT 12
US-10-241-220-44
; Sequence 44, Application US/10241220
; Publication No. US20030148408A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/241,220
; CURRENT FILING DATE: 2002-12-13
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-241-220-44

Query Match 87.6%; Score 754.2; DB 15; Length 1850;
Best Local Similarity 98.3%; Pred. No. 3.3e-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTGTGTTCCAGAGCATCGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGT 146
DB 77 TCTCTCGGAACAGGCAATGGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGT 136
QY 147 GGTGATGATGGTGTGATGATCAGTGCTGCTGAGCCACTTACAGCTGTCTGC 206
DB 137 GGTGATGATGGTGTGATGATCAGTGCTGCTGAGCCACTTACAGCTGTCTGC 196
QY 207 ACGGTCTTCATCAGCGGCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGA 266
DB 197 ACGGTCTTCATCAGCGGCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGA 256
QY 267 AGATGCTGTGGCCCTCGAGAGGACAGTGTCCAGCAACGGAATCCAGAGCGGAGGT 326
DB 257 AGATGCTGTGGCCCTCGAGAGGACAGTGTCCAGCAACGGAATCCAGAGCGGAGGT 316
QY 327 CTACGCGCCGCTCGGCCACCGACCGCTGGCGCTGCCGCCCTTCGCCAGCGGAGCG 386
DB 317 CTACGCGCCGCTCGGCCACCGACCGCTGGCGCTGCCGCCCTTCGCCAGCGGAGCG 376
QY 387 CTTTCCACCGCTTCAGGCCCACTTATCCGTAACCTGACGACAGATCGAAGCTGCCAC 446
DB 377 CTTTCCACCGCTTCAGGCCCACTTATCCGTAACCTGACGACAGATCGAAGCTGCCAC 436
QY 447 CATCTGCTGTGAGAGGGGAGAGGCCCCACCTTACAGGGGCCCTGACCCCTCAGCT 506
DB 437 CATCTGCTGTGAGAGGGGAGAGGCCCCACCTTACAGGGGCCCTGACCCCTCAGCT 496

QY 507 TCGGGAACCCGAGCAGCAGCTGGAACCTGAACCCGGGAGTGGTGGGGGACCCCCAACAG 566
DB 497 TCGGGAACCCGAGCAGCAGCTGGAACCTGAACCCGGGAGTGGTGGGGGACCCCCAACAG 556
QY 567 AACCATCTTCGACAGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCCAG 626
DB 557 AACCATCTTCGACAGTGACCTGATGATAGTGCAGGCTGGGGGGCCCTGCCCCCCAG 616
QY 627 CAGTAACTCGGGCATCAGGCGCCACGCTGCTACGCGAGCGGGCGGCGCATGAGGGGCGGCC 686
DB 617 CAGTAACTCGGGCATCAGGCGCCACGCTGCTACGCGAGCGGGCGGCGCATGAGGGGCGGCC 676
QY 687 GCCCACCCTACAGGAGGTCATCGGCCCACTACCCGGGGTCTCTCTCCAGCACCAGCAGAG 746
DB 677 GCCCACCCTACAGGAGGTCATCGGCCCACTACCCGGGGTCTCTCTCCAGCACCAGCAGAG 736
QY 747 CAGTGGGCGCCCTCTCTGCTGGAGGGGACCCGGCTCCACACACACATCGGGCCCT 806
DB 737 CAGTGGGCGCCCTCTCTGCTGGAGGGGACCCGGCTCCACACACACATCGGGCCCT 796
QY 807 AGAGGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 861
DB 797 AGAGGCGCAGCCATCTGGAGCAAGAGAGGATTAACAGAAAGGACACCCCTCTC 851

RESULT 13
US-10-872-972-44
; Sequence 44, Application US/10872972
; Publication No. US20040229277A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF TUMOR
; FILE REFERENCE: P5010R1-US
; CURRENT APPLICATION NUMBER: US/10/872,972
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIOR FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 44
; LENGTH: 1850
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-872-972-44

Query Match 87.6%; Score 754.2; DB 18; Length 1850;
Best Local Similarity 98.3%; Pred. No. 3.3e-191;
Matches 762; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 87 TTGTGTTCCAGAGCATCGAGATCAGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGT 146
DB 77 TCTCTCGGAACAGGCAATGGGAGCTGGAGTTGTTTCAGATCATCATCTCGTGT 136
QY 147 GGTGATGATGGTGTGATGATGATCAGTGCTGCTGAGCCACTTACAGCTGTCTGC 206
DB 137 GGTGATGATGGTGTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 196
QY 207 ACGGTCTTCATCAGCGGCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGA 266
DB 197 ACGGTCTTCATCAGCGGCACAGCCAGGGCGGAGAGAGATGCCCTGTCTCAGA 256
QY 267 AGATGCTGTGGCCCTCGAGAGGACAGTGTCCAGCAACGGAATCCAGAGCGGAGGT 326
DB 257 AGATGCTGTGGCCCTCGAGAGGACAGTGTCCAGCAACGGAATCCAGAGCGGAGGT 316

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 10:31:50 ; Search time 2707.69 Seconds
(without alignments)
12103.794 Million cell updates/sec

Title: US-09-934-249-3
Perfect score: 861
Sequence: 1 atgcacgcttgatgggggt.....aacagaaaggacacccctctc 861

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST.*

1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	811.8	94.3	1005	1	AL578575
c 2	807.6	93.8	1038	1	AL517150
c 3	743.6	86.4	967	5	BQ641849
c 4	700	81.3	1046	5	BM922276
c 5	693	80.5	901	3	CR612083
c 6	687.8	79.9	945	5	BQ532219
c 7	686.2	79.7	850	1	AL558881
c 8	667.4	77.5	916	5	BQ954555
c 9	667	77.5	867	5	BX362396
c 10	666.6	77.4	897	1	AL558882
c 11	662.8	77.0	850	5	BQ602918
c 12	648	75.3	780	9	AY419334
c 13	614.6	71.4	1079	3	BC023092
c 14	607.4	70.5	609	5	BQ636742
c 15	603.6	70.1	1207	3	AK008976
c 16	588.8	68.4	605	7	CV028567
c 17	578.4	67.2	890	5	BQ690750
c 18	570.4	66.2	973	5	BUI69156
c 19	568.8	66.1	572	5	BX641317
c 20	568.2	66.0	782	5	BQ015170
c 21	550	63.9	551	4	BM141979
c 22	529.8	61.5	894	4	BI851941
c 23	519.4	60.3	729	5	BQ575741
c 24	516.8	60.0	730	4	BM677602

c 25	515.2	59.8	728	5	BU683523	BU683523	UI-CF-BC1
c 26	504	58.5	780	9	AY419335	AY419335	Pan trogl
c 27	501.6	58.3	588	4	BM483503	BM483503	536869 MA
c 28	487.8	56.7	1059	1	AL543170	AL543170	AL543170
c 29	487.6	56.6	646	9	CG784226	CG784226	FHRC-GT-
c 30	475.2	55.2	624	9	AY419336	Mus muscu	AY419336
c 31	468	54.4	857	4	BG323347	BG323347	602421734
c 32	465.8	54.1	744	5	BU414421	BU414421	603670223
c 33	461	53.5	763	4	BI646175	BI646175	603276395
c 34	445.6	51.8	693	1	AI761441	AI761441	wg65f07.x
c 35	445.4	51.7	655	5	BQ691705	BQ691705	AGENCOURT
c 36	445.4	51.7	1280	5	BQ691500	BQ691500	AGENCOURT
c 37	443.6	51.5	651	6	CB554226	CB554226	MMSPO052
c 38	440	51.1	899	5	BUI69912	BUI69912	AGENCOURT
c 39	432.8	50.3	964	5	BUI59860	BUI59860	AGENCOURT
c 40	430	49.9	841	4	BI156703	BI156703	602922119
c 41	429.6	49.9	646	5	BUI59841	BUI59841	AGENCOURT
c 42	428.8	49.8	974	2	BB624904	BB624904	BB624904
c 43	428.2	49.7	655	4	BI853324	BI853324	603379903
c 44	416.2	48.3	587	4	BI083462	BI083462	602875788
c 45	411.6	47.8	1127	5	BUI74654	BUI74654	AGENCOURT

ALIGNMENTS

RESULT 1
AL578575/c
LOCUS
DEFINITION
AL578575 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CSODK001YC24 3-PRIME, mRNA sequence.
ACCESSION
AL578575
VERSION
AL578575.3
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
1 (bases 1 to 1005)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
JOURNAL
On Feb 16, 2001 this sequence version replaced gi:31316780.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen. This sequence belongs to sequence cluster
9945.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSODK001B12NP1&c=9945.r.

FEATURES
source

1. 1005
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODK001YC24"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/notes="Homo sapiens HELA CELLS COT 25-NORMALIZED"
/notes="1st strand cDNA was primed with a NotI-oligo(dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 94.3%; Score 811.8; DB 1; Length 1005;
Best Local Similarity 97.7%; Pred. No. 9.9e-170;
Matches 835; Conservative 8; Mismatches 10; Indels 2; Gaps 2;


```
QY 349 GACCGCTGCGCTGCGCGCCCTTCGCCGCCAGGGAGGGCTTCACCGCTTCAGCCGCCACC 408
Db 181 GACCGCTGCGCTGCGCGCCCTTCGCCGCCAGGGAGGGCTTCACCGCTTCAGCCGCCACC 240
QY 409 TATCCGTACTGTCAGCAGCAGAGTGCACCTCCACCCACCACTATCTGCTGTCAGACGGGGAG 468
Db 241 TATCCGTACTGTCAGCAGCAGAGTGCACCTCCACCCACCACTATCTGCTGTCAGACGGGGAG 300
QY 469 GAGCCCCCACCCTACACAGGCGCCCTGCACCCCTCAGCTTCGGGACCCCGAGCAGCAGCTG 528
Db 301 GAGCCCCCACCCTACACAGGCGCCCTGCACCCCTCAGCTTCGGGACCCCGAGCAGCAGCTG 360
QY 529 GAATGAAACCGGAGTGGTGGGGGCAACCCGCAACGAAACCACTCTTCGACAGTGCAGCTG 588
Db 361 GAATGAAACCGGAGTGGTGGGGGCAACCCGCAACGAAACCACTCTTCGACAGTGCAGCTG 420
QY 589 ATGGATAGTCCAGAGCTGGGCGGCCCTGCGCCCGCCCGCCAGCAGTAACTCGGGCATCAGCGCC 648
Db 421 ATGGATAGTCCAGAGCTGGGCGGCCCTGCGCCCGCCCGCCAGCAGTAACTCGGGCATCAGCGCC 480
QY 649 ACCTGCTACCGCAGCGCGCGCGCATGGAGGGCGCGCGCCCGCCACCTACACGAGAGTCAATC 708
Db 481 ACCTGCTACCGCAGCGCGCGCGCATGGAGGGCGCGCGCGCCCGCCACCTACACGAGAGTCAATC 540
QY 709 GGCACACTACCGGGGTCTCTTCAGCAGCAGCAGCAGTGGGGCGCGCGCTCTCTTGTCTG 768
Db 541 GGCACACTACCGGGGTCTCTTCAGCAGCAGCAGCAGTGGGGCGCGCGCTCTCTTGTCTG 600
QY 769 GAGGGGACCGGGTCCACACACACACATCGCGCCCTAGAGAGCGCGCATCTCGGAGC 828
Db 601 GAGGGGACCGGGTCCACACACACACATCGCGCCCTAGAGAGCGCGCATCTCGGAGC 660
QY 829 AAAGAGAGGATAAACAGAAAGACACCTCTC 861
Db 661 AAAGAGAGGATAAACAGAAAGACACCTCTC 693
```

RESULT 6

```
BU539219
LOCUS BU539219 945 bp mRNA linear EST 13-SEP-2002
DEFINITION AGENCOURT 10215265 NIH_MGC_107 Homo sapiens cDNA clone
IMAGE:6569922 5', mRNA sequence.
```

ACCESSION BU539219

VERSION BU539219.1 GI:22849660

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 945)

NIH-MGC <http://mgs.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

<http://image.llnl.gov>

Plate: LLCM2757 row: p column: 18

High quality sequence stop: 563.

Location/Qualifiers

1..945

FEATURES

source

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6569922"

/tissue_type="adenocarcinoma, cell line"

/lab_host="DH10B (phage-resistant)"

RESULT 7

AL558881/c

LOCUS

DEFINITION

AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED

Homo sapiens cDNA clone CS0J015YF12 3-PRIME, mRNA sequence.

850 bp mRNA linear EST 02-APR-2004

AL558881

Homo sapiens

cDNA clone CS0J015YF12 3-PRIME, mRNA sequence.

850 bp mRNA linear EST 02-APR-2004

/clone lib="NIH_MGC_107"
/notes="Organ: breast; Vector: pOTB7; Site: 1: EcoRI;
Site 2: XhoI; cDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGACAGAG(G). Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN

```
Query Match 79.9%; Score 687.8; DB 5; Length 945;  
Best Local Similarity 96.6%; Pred. No. 3.4e-142;  
Matches 734; Conservative 0; Mismatches 23; Indels 3; Gaps 3;  
QY 87 TTGTGTTCCAGAGCATCGAGATCACGGAGCTGAGATTGTTTCAGATCATCATCGTGGT 146  
Db 65 TCTCTCGGAACACAGGCAATCGGAGCTGGAGTTGTTTCAGATCATCATCGTGGT 124  
QY 147 GGTGATGATGTTGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 206  
Db 125 GGTGATGATGTTGATGTTGTTGATGATGATGATGATGATGATGATGATGATGATGATG 184  
QY 207 ACCTGCTTTCATCAGCGCGCACAGCGCGGAGGAGAGAGATGCGCTGTCTCTCAGA 266  
Db 185 ACCTGCTTTCATCAGCGCGCACAGCGCGGAGGAGAGAGATGCGCTGTCTCTCAGA 244  
QY 267 AGATGCTGTGTCGCTTCGGAGAGCAGTGTTCAGGCAACGGAATCCAGAGCGCGAGGT 326  
Db 245 AGATGCTGTGTCGCTTCGGAGAGCAGTGTTCAGGCAACGGAATCCAGAGCGCGAGGT 304  
QY 327 CTACGCGCGCGCTTCGGCGCCACCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCG 386  
Db 305 CTACGCGCGCGCTTCGGCGCCACCGCGCTGCGCGCTGCGCGCTGCGCGCTGCGCGCG 364  
QY 387 CTTCACCGCTTCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 446  
Db 365 CTTCACCGCTTCACGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 424  
QY 447 CATCTCGCTTCAGAGCGGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 506  
Db 425 CATCTCGCTTCAGAGCGGGAGGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 484  
QY 507 TCGGAGACCGCGAGCAGAGCTGGAATGAAACCGGGAGTGGTGGCGGCAACCCCAACAG 566  
Db 485 TCGGAGACCGCGAGCAGAGCTGGAATGAAACCGGGAGTGGTGGCGGCAACCCCAACAG 544  
QY 567 AACCATCTTCGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 626  
Db 545 AACCATCTTCGACAGTACCTGATGATGATGATGATGATGATGATGATGATGATGATG 604  
QY 627 CAGTAACCTCGGGCATCAGCGCCACGTCGTACGGCAGCGCGCGCGCGCGCGCGCGCGCG 686  
Db 605 CAGTAACCTCGGGCATCAGCGCCACGTCGTACGGCAGCGCGCGCGCGCGCGCGCGCGCG 664  
QY 687 GCCCACTACAGCAGAGTCAATCGGCGCACTACCGGGGTCTCTTCAGACCAACAGAGAG 746  
Db 665 GCCCACTACAGCAGAGTCAATCGGCGCACTACCGGGGTCTCTTCAGACCAACAGAGAG 724  
QY 747 CAGTGGCGCGCGCTTCCTTCTGAGGGGACCGCGCTCCACACACACACATCGCG-CCC 804  
Db 725 CAGTGGCGCGCGCTTCCTTCTGAGGGGACCGCGCTCCACACACACACATCGCG-CCC 784  
QY 805 CTAGAGAGCGCAG-CCATCTGAGAGCAAGAGAGAGAGTAA 843  
Db 785 CTAGAGAGCGCAGCCCATCTGAGAGCAAGAGAGAGTAA 824
```

RESULT 7

AL558881/c

LOCUS

DEFINITION

AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED

Homo sapiens cDNA clone CS0J015YF12 3-PRIME, mRNA sequence.

850 bp mRNA linear EST 02-APR-2004

AL558881

Homo sapiens

cDNA clone CS0J015YF12 3-PRIME, mRNA sequence.

850 bp mRNA linear EST 02-APR-2004

ACCESSION AL558881
 VERSION AL558881.3 GI:46184268
 EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 850)
 AUTHORS Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
 TITLE Full-length cDNA libraries and normalization
 JOURNAL Unpublished (2001)
 COMMENT On Feb 15, 2001 this sequence version replaced gi:31283014.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0D015DC06NP1&c=9945.r.
 FEATURES
 Location/Qualifiers
 1..850
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0D015YF12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /cell_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."
 ORIGIN
 Query Match 79.7%; Score 686.2; DB 1; Length 850;
 Best Local Similarity 99.3%; Pred. No. 7.6e-142;
 Matches 688; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 169 GTGATCAGCGCTGCTGAGCCACTCAAGCTGTCTGCAGCGTCCCTTCATCAGCCGGAC 228
 DB 850 GTGTCAGCTGCTGCTGAGCCACTCAAGCTGTCTGCAGCGTCCCTTCATCAGCCGGAC 791
 QY 229 AGCCAGGGCGGAGGAGAGATGCGCTGTCTCAGAGAGATGCTGTGGCCCTCGGAG 288
 DB 790 AGCCAGGGCGGAGGAGAGATGCGCTGTCTCAGAGAGATGCTGTGGCCCTCGGAG 731
 QY 289 AGCAGAGTGTGAGGCAACGAATCCAGAGCGCGAGTCTACGCCCGCTCGGCCACC 348
 DB 730 AGCAGAGTGTGAGGCAACGAATCCAGAGCGCGAGTCTACGCCCGCTCGGCCACC 671
 QY 349 GACCGCTGCGCTGCGCCCTTCGCCCCAGCGGAGCGCTTCACCGCTTCCAGGCCACC 408
 DB 670 GACCGCTGCGCTGCGCCCTTCGCCCCAGCGGAGCGCTTCACCGCTTCCAGGCCACC 611
 QY 409 TATCCGTACTGACGACGAGATCGACTCTGACCCACCCACCATCTCGTGTGACAGCGGAG 468
 DB 610 TATCCGTACTGACGACGAGATCGACTCTGACCCACCCACCATCTCGTGTGACAGCGGAG 551
 QY 469 GAGCCCCACCCCTACGAGCGCCCTTCGACCTTCAGCTTCGGGACCCCGAGCAGAGCTG 528
 DB 550 GAGCCCCACCCCTACGAGCGCCCTTCGACCTTCAGCTTCGGGACCCCGAGCAGAGCTG 491
 QY 529 GAACTGAAACCGGAGTGTGTCGCGCACCCCAAAACAGAACCATCTTCGACAGTGCCTG 588
 DB 490 GAACTGAAACCGGAGTGTGTCGCGCACCCCAAAACAGAACCATCTTCGACAGTGCCTG 431
 QY 589 ATGGATAGTGCCAGGCTGGGGCGGCCCTTGCCTCCCGCCAGCAGTAGTAACTCGGGCATCAGCGCC 648

Db 430 ATGGATAGTGCCAGGCTGGGGCGGCCCTTGCCTCCCGCCAGCAGTAACTCGGGCATCAGCGCC 371
 QY 649 ACCTGTCTACGGCAGCGCGCGGCATGTGAGGGCGGCCCGCCACCTACAGCGAGGTATC 708
 Db 370 ACCTGTCTACGGCAGCGCGCGGCATGTGAGGGCGGCCCGCCACCTACAGCGAGGTATC 311
 QY 709 GGCCACTACCCCGGGTCCCTCTCCAGACACACAGAGCAGTGGGCGGCCCTCTTGGTG 768
 Db 310 GGCCACTACCCCGGGTCCCTCTCCAGACACACAGAGCAGTGGGCGGCCCTCTTGGTG 251
 QY 769 GAGGGACCGCGCTCCACACACACATCGCGCCCTAGAGAGCGCAGCATCTCGAGC 828
 Db 250 GAGGGACCGCGCTCCACACACACATCGCGCCCTAGAGAGCGCAGCATCTCGAGC 191
 QY 829 AAGAGAGAGATAAACAGAAAGACACCTCTC 861
 Db 190 AAGAGAGAGATAAACAGAAAGACACCTCTC 158
 RESULT 8
 LOCUS BQ954555
 DEFINITION AGENCOURT 8825282 Lupski sciatic_nerve Homo sapiens cDNA clone
 IMAGE:6204609 5', mRNA sequence.
 ACCESSION BQ954555
 VERSION BQ954555.1 GI:22370033
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 916)
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue procurement: Dr. James R. Lupski
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLNL1626 row: c column: 10
 High quality sequence stop: 669.
 Location/Qualifiers
 1..916
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6204609"
 /sex="male"
 /tissue_type="sciatic nerve"
 /dev_stage="adult, 70 yr"
 /lab_host="DH10B"
 /clone_lib="Lupski sciatic_nerve"
 /note="Vector: pCMV-SF016 (Life Technologies); Site_1: NotI; Site_2: SalI; cDNA made by oligo-dT priming. Directionally cloned using the following adaptors: 5'-TCGACCCACCGGTCCG-3' and 5'-GACTAGTTCTAGATCGGAGCGGCCCT(15)-3'. Size selected > 1 kb for average insert length 1.87 kb. This is a primary library, non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life Technologies."
 ORIGIN
 Query Match 77.5%; Score 667.4; DB 5; Length 916;
 Best Local Similarity 95.3%; Pred. No. 1.1e-137;
 Matches 731; Conservative 0; Mismatches 31; Indels 5; Gaps 4;

QY 810 GAGCCACCCATCTGGAGCAAGAGAGATATAACAGAAAGGACACCCCTCTC 861
 |||||
 Db 208 GAGCGACCCATCTGGAGCAAGAGAGATATAACAGAAAGGACACCCCTCTC 157
 |||||

RESULT 10
 AL558882 897 bp mRNA linear EST 02-APR-2004
 LOCUS AL558882 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CS0DJ015VF12 5-PRIME, mRNA sequence.
 ACCESSION AL558882
 VERSION AL558882.3 GI:46184269
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE
 AUTHORS Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 TITLE Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 JOURNAL 1 (bases 1 to 897)
 COMMENT Li, W.B., Gruber, C., Jesse, J., and Polayes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31283015.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library is constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.r

For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?s=CS0DJ015DC06QP1&c=9945.r.

FEATURES
 source
 Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ015VF12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /call_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /notes="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN
 Query Match 77.4%; Score 666.6; DB 1; Length 897;
 Best Local Similarity 99.3%; Pred. No. 1.7e-137;
 Matches 688; Conservative 2; Mismatches 1; Indels 2; Gaps 2;
 169 GTGATCAGCGTCTGTGACCACTACAGCTGTGCGCGTCTTATCAGCGGCAC 228
 1 GTGATCAGCGTCTGTGACCACTACAGCTGTGCGCGTCTTATCAGCGGCAC 60
 229 AGCCAGGGCGGAGGAGAGATGCCCTGCTCTCAGAGAGATGCTGTGGCCCTCGGAG 288
 61 AGCCAGGGCGGAGGAGAGATGCCCTGCTCTCAGAGAGATGCTGTGGCCCTCGGAG 120
 289 AGCACAGTGTACGGCAACGAATCCAGAGCGCGAGTCTAGCGCCGCTCGGCCACC 348
 121 AGCACAGTGTACGGCAACGAATCCAGAGCGCA-GTCTAGCGCCGCTCGGCCACC 179
 349 GACCGCTGGCGTGGCGCTTCGCCGACGCGGAGCGCTTCAACGCTTCAGGCCACC 408
 180 GACCGCTGGCGTGGCGCTTCGCCGACGCGGAGCGCTTCAACGCTTCAGGCCACC 239
 409 TATCCGTACTGTGACGACGAGATCGACCTGGCCACCACCATCTCGCTGTGACGCGGAG 468
 |||||

Db 240 TATCCGTACTCTGAGCAGCAGATCGACCTCGGCCACCATCTCGCTGTGACGGGGAG 299
 QY 469 GAGCCCCCACTTACACAGGGCCCTTGACACCTTGAGCTTCGGGACCCCGAGCGAGCTG 528
 Db 300 GAGCCCCCACTTACACAGGGCCCTTGACACCTTGAGCTTCGGGACCCCGAGCGAGCTG 359
 QY 529 GAATCTGAACCGGAGTGGTGGCGCACCCCAAGAACCAACCATCTTCGACAGTGACCTG 588
 Db 360 GAATCTGAACCGGAGTGGTGGCGCACCCCAAGAACCAACCATCTTCGACAGTGACCTG 419
 QY 589 ATGATAGTATCCAGAGTGGCGGCCCTTGCCGCCCCAGCAGTAACTCGGGCCTACAGCGCC 648
 Db 420 ATGATAGTATCCAGAGTGGCGGCCCTTGCCGCCCCAGCAGTAACTCGGGCCTACAGCGCC 479
 QY 649 ACCTGTCTACGGCAGCGCGGCCCATGAGGGCGCCGCCACCTTACAGCGAGTCAATC 708
 Db 480 ACCTGTCTACGGCAGCGCGGCCCATGAGGGCGCCGCCACCTTACAGCGAGTCAATC 539
 QY 709 GGCACCTTACCCGGGGTCTCTCTTCCAGCAGCAGCAGCAGTGGCGGCCCTCTTGTCTG 768
 Db 540 GGCACCTTACCCGGGGTCTCTCTTCCAGCAGCAGCAGCAGTGGCGGCCCTCTTGTCTG 599
 QY 769 GAGGGAGCCCGGCTCCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGC 828
 Db 600 GAGGGAGCCCGGCTCCACACACATCGCGCCCTAGAGAGCGCA-SCATCTGGAGC 658
 QY 829 AAAGAGAAGGATAAACAAGAAAGACACCCCTCTC 861
 Db 659 AAAGAGAAGGATAAACAAGAAAGACACCCCTCTC 691
 |||||

RESULT 11
 BU602918 850 bp mRNA linear EST 20-SEP-2002
 LOCUS AGENCOURT_10016502 NIH_MGC_142 Homo sapiens cDNA clone
 DEFINITION IMAGE:6497853 5', mRNA sequence.
 ACCESSION BU602918
 VERSION BU602918.1 GI:23254677
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 AUTHORS NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs@mail.nih.gov
 Tissue Procurement: NCI
 cDNA Library Preparation: Michael Brownstein Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2679 row: 1 column: 22
 High quality sequence stop: 499.
 Location/Qualifiers
 1..850
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6497853"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC_142"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattggcc);
 Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2% blood - 33.4% brain - 5.6% breast - 12.5% colon -
 4% connective tissue - 1.4% eye - 1% intestine - 2.6%
 kidney - 2.2% liver - 5.7% lung - 10.8% NK-cell - 5.2%,"

FEATURES
 source
 Location/Qualifiers
 1..850
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6497853"
 /tissue_type="mixed (pool of 40 RNAs)"
 /lab_host="DH10B (T1-phage-resistant)"
 /clone_lib="NIH MGC_142"
 /note="Vector: pDNR-LIB; Site 1: SfiI (ggccattggcc);
 Site 2: SfiI (ggcgctcgcc); Double-stranded cDNA was
 prepared from a pool of 40 cell line polyA+ RNAs (bladder
 - 2% blood - 33.4% brain - 5.6% breast - 12.5% colon -
 4% connective tissue - 1.4% eye - 1% intestine - 2.6%
 kidney - 2.2% liver - 5.7% lung - 10.8% NK-cell - 5.2%,"

Result No.	Score	Query #			ID	Description
		Match	Length	DB		
1	861	100.0	861	6	AX392419	Sequence
2	861	100.0	1321	6	AX392417	Sequence
3	861	100.0	4839	6	CQ812357	Sequence
4	861	100.0	4839	9	AF305616	Homo sapi
5	810	94.1	1383	6	AX775889	Sequence
6	790	91.8	1061	9	BC015918	Homo sapi
7	752	87.3	759	6	AR336831	Sequence
8	752	87.3	1140	6	AR336830	Sequence
9	752	87.3	1141	9	AF224278	Homo sapi
10	752	87.3	1818	9	AY128643	Homo sapi
11	701	81.4	753	6	BD272534	Secrated
12	701	81.4	756	6	BD272495	Secrated
13	701	81.4	759	6	BD272545	Secrated
14	701	81.4	969	6	BD272494	Secrated
15	701	81.4	1085	6	AX775887	Sequence
16	701	81.4	1913	6	BD272544	Secrated
17	696	80.8	969	6	BD272514	Secrated
18	650	75.5	969	6	BD272515	Secrated
19	650	75.5	969	6	BD272516	Secrated

Qy	481	TACAGGGCCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG	540
Db	801	TACAGGGCCCCCTGCACCTCCAGCTTCGGGACCCCGAGCAGCAGCTGGAACTGAACCGG	860
Qy	541	GAGTCGGTGGCGCACCCCAACAGACACCATCTTCGACAGTCACTGATGATAGTGC	600
Db	861	GAGTCGGTGGCGCACCCCAACAGACACCATCTTCGACAGTCACTGATGATAGTGC	920
Qy	601	AGGCTGGGGGGCCCCCTGCGCCCCCAGCAGTAACTCGGGCATCAGCGCCACTGCTACGGC	660
Db	921	AGGCTGGGGGGCCCCCTGCGCCCCCAGCAGTAACTCGGGCATCAGCGCCACTGCTACGGC	980
Qy	661	AGCGGGGGCGCATGAGAGGGCGCGCCCACTACAGCGAGTCACTCGGCCACTACCCG	720
Db	981	AGCGGGGGCGCATGAGAGGGCGCGCCCACTACAGCGAGTCACTCGGCCACTACCCG	1040
Qy	721	GGTCTCTCTTCAGACACAGCAGAGCAGTGGGGCCCTCTTCTGCGAGGGGACCCCG	780
Db	1041	GGTCTCTCTTCAGACACAGCAGAGCAGTGGGGCCCTCTTCTGCGAGGGGACCCCG	1100
Qy	781	CTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAAGAT	840
Db	1101	CTCCACCACACACATCGCGCCCTAGAGAGCGCAGCCATCTGGAGCAAGAGAAGAT	1160
Qy	841	AAACAGAAAGGACACCTCTCTC	861
Db	1161	AAACAGAAAGGACACCTCTCTC	1181
RESULT 4			
AF305616			
LOCUS	Homo sapiens STAG1/PMEP1 mRNA, complete cds.		
DEFINITION	Homo sapiens STAG1/PMEP1 mRNA, complete cds.		
ACCESSION	AF305616		
VERSION	AF305616.1 GI:16303741		
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.		
JOURNAL	1 (bases 1 to 4839)		
MEDLINE	Characterization of a novel gene, STAG1/PMEP1, upregulated in		
PUBMED	renal cell carcinoma and other solid tumors		
AUTHORS	Mol. Carcinog. 32 (1), 44-53 (2001)		
TITLE	21453682		
JOURNAL	11568975		
MEDLINE	2 (bases 1 to 4839)		
PUBMED	Rae, F.K., Hooper, J.D., Nicol, D.L. and Clements, J.A.		
AUTHORS	Direct Submission		
TITLE	Submitted (14-SEP-2000) Centre for Molecular Biotechnology,		
JOURNAL	Queensland University of Technology, 2 George St, Brisbane, QLD		
FEATURES	4001, Australia		
source	Location/Qualifiers		
	1. .4839		
	/organism="Homo sapiens"		
	/mol_type="mRNA"		
	/db_xref="taxon:9606"		
	/chromosome="20"		
	/map="20q13.2-q13.33"		
	321. .1184		
	/note="unknown function"		
	/codon_start=1		
	/product="STAG1/PMEP1"		
	/protein_id="AA116781.1"		
	/db_xref="GI:16303742"		
	/translation="MRLMGVNSTAAAGAGQNVCTCKRSLFQSMETTELEFVQI		
	IIVVVMVWVIVLCLSHYKLSBFSIRHSQGRREDALSSSECLWPSSSTVSGN		
	GIPEQVAPPRDLRVLPPPAQRFRHFQTYPLDHEIDLPPTLSLDEEPPFP		
	YQFCFTLDQPEQLEARNRAPPNRTIFDSDLMSARLGGPCPPSSNSGISATV		
	YSGSGRMGEPPPTYSVIGHYGSSFPQHQSGPPSLLEGTTLRHHTHIAPLESAAIV		
	KENDKQKQKHPH"		
CDS			

[illegible]

PR	01-MAR-1999 US	60/122458
PI	THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER	
PC	C12N15/09, C07K14/47, C07K16/18, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15,	
PC	G01N33/50, G01N33/53, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC	
	Secreted proteins and nucleic acids encoding them PH Key	
	Location/Qualifiers	
FT	source	1..753
FT	source	/organism='Homo sapiens (human)'. Location/Qualifiers 1..753 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606"
FEATURES	source	
ORIGIN		
	Query Match	81.4%; Score 701; DB 6; Length 753;
	Best Local Similarity	99.9%; Pred. No. 0;
	Matches 75;	Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy	110 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTTGGTGAATGATGATGATGTTGGTGG 169	
Db	2 CGGAGCTGGAGTTTGTTCAGATCATCATCATCGTGTTGGTGAATGATGATGATGTTGGTGG 61	
Qy	170 TGATCAGTGTGCTCTGAGCCACTACAACTGTCTGCACGGTCTTTATCAGCCGGCACCA 229	
Db	62 TGATCAGTGTGCTCTGAGCCACTACAACTGTCTGCACGGTCTTTATCAGCCGGCACCA 121	
Qy	230 GCCAGGGCGGAGGAGAGAGATGCCCTGTCTCTCAGAAGGATGCTGTGGCCCCCTCGGAGA 289	
Db	122 GCCAGGGCGGAGGAGAGATGCCCTGTCTCTCAGAAGGATGCTGTGGCCCCCTCGGAGA 181	
Qy	290 GCACAGTGTCAAGCAACGGTAATCCCAGAGCCGACAGGCTTAGCCCCGCCCTCGGCCACC 349	
Db	182 GCACAGTGTCAAGCAACGGTAATCCCAGAGCCGACAGGCTTAGCCCCGCCCTCGGCCACC 241	
Qy	350 ACCGCTTGGCGTGCCTCCCTTCGCCCCAGCGGGAGCGCTTCCACGGCTTCCAGCCCACT 409	
Db	242 ACCGCTTGGCGTGCCTCCCTTCGCCCCAGCGGGAGCGCTTCCACGGCTTCCAGCCCACT 301	
Qy	410 ATCCGTACTTGCACGACGAGATGCACCTGCCACCCACCATCTCGCTGTCTCAGACGGGGAG 469	
Db	302 ATCCGTACTTGCACGACGAGATGCACCTGCCACCCACCATCTCGCTGTCTCAGACGGGGAG 361	
Qy	470 AGCCCCCACTTACAGGGCCCCCTTGACCTTCAAGTTCGGGACCCCGAGCAGCAGCTGG 529	
Db	362 AGCCCCCACTTACAGGGCCCCCTTGACCTTCAAGTTCGGGACCCCGAGCAGCAGCTGG 421	
Qy	530 AACCTAACCCGGGAGTTCGGTGGCGGCACCCCAACAGAACCATCTTCGACAGTGAACCTGA 589	
Db	422 AACCTAACCCGGGAGTTCGGTGGCGGCACCCCAACAGAACCATCTTCGACAGTGAACCTGA 481	
Qy	590 TGGATAGTGCACAGCTGGGGCGGCCCTTGCCCCCGCCAGCAGTAACCTCGGGGATCAGCGCCA 649	
Db	482 TGGATAGTGCACAGCTGGGGCGGCCCTTGCCCCCGCCAGCAGTAACCTCGGGGATCAGCGCCA 541	
Qy	650 CGTGCTACGGCAGCGGGGGCGCATAGAGGGGGCGCCGCCCACTTACAGCGAGGTATCG 709	
Db	542 CGTGCTACGGCAGCGGGGGCGCATAGAGGGGGCGCCGCCCACTTACAGCGAGGTATCG 601	
Qy	710 GCCACTACCCGGGTCTCTCTTCAGACACAGCAGACAGTGGGGCGCCCTCTTGTCTGG 769	
Db	602 GCCACTACCCGGGTCTCTCTTCAGACACAGCAGACAGTGGGGCGCCCTCTTGTCTGG 661	
Qy	770 AGGGGACCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 829	
Db	662 AGGGGACCCGGCTCCACACACACACATCGCGCCCTTAGAGAGCGCAGCCATCTGGAGCA 721	
Qy	830 AAGAGAGGGATAAACAAGAAAGGACACCCCTCTC 861	
Db	722 AAGAGAGGGATAAACAAGAAAGGACACCCCTCTC 753	

	ORIGIN	/ad_xref=taxon:9606"
Query Match	81.4%;	Score 701; DB 6; Length 759;
Best Local Similarity	99.9%;	Pred. No. 0;
Matches 751;	Conservative 0;	Mismatches 1; Indels 0; Gaps 0;
OY	110	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGCGTGCATCATGTGATGTGTGTGG 169
Ddb	5	CGGAGCTGGAGTTTGTTCAGATCATCATCGTGCGTGCATCATGTGATGTGTGTGG 64
OY	170	TGATCAGTGCCCTGCTGAGCCACTCAAGCTGTCTGCACGTCCTTCATCAGCGCGACA 229
Ddb	65	TGATCAGTGCCCTGCTGAGCCACTCAAGCTGTCTGCACGTCCTTCATCAGCGCGACA 124
OY	230	GCCAGGGCGGAGAGAAGATGCCCTGTCTCAGAAGGATGCCCTGTGCCCTCGGAGA 289

COMMENT	
MILLENNIUM PHARMACEUTICALS INC	
OS Homo sapiens (human)	
PN JP 2002539773-A/3	
PD 26-NOV-2002	
PF 01-MAR-2000 JP 2000603247	
PR 01-MAR-1999 US 60/122458	
PI THOMAS M BARNES, DOUGLAS A HOLTZMAN, JOHN D SHARP, CHRISTOPHER C FRASER	
PC C12N15/09, C07K14/47, C07K16/13, C12N5/10, C12P21/02, C12Q1/68, PC G01N33/15,	
PC G01N33/50, G01N33/53, G01N33/56, C12N15/00, C12N5/00 CC	
Secrated proteins and nucleic acids encoding them FH Key	
Location/Qualifiers	
CDS (6). .(761).	
FT Location/Qualifiers	
FEATURES	

REFERENCE	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	
-----------	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

REFERENCE	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	101	102	103	104	105	106	107	108	109	110	111	112	113	114	115	116	117	118	119	120	121	122	123	124	125	126	127	128	129	130	131	132	133	134	135	136	137	138	139	140	141	142	143	144	145	146	147	148	149	150	151	152	153	154	155	156	157	158	159	160	161	162	163	164	165	166	167	168	169	170	171	172	173	174	175	176	177	178	179	180	181	182	183	184	185	186	187	188	189	190	191	192	193	194	195	196	197	198	199	200	201	202	203	204	205	206	207	208	209	210	211	212	213	214	215	216	217	218	219	220	221	222	223	224	225	226	227	228	229	230	231	232	233	234	235	236	237	238	239	240	241	242	243	244	245	246	247	248	249	250	251	252	253	254	255	256	257	258	259	260	261	262	263	264	265	266	267	268	269	270	271	272	273	274	275	276	277	278	279	280	281	282	283	284	285	286	287	288	289	290	291	292	293	294	295	296	297	298	299	300	301	302	303	304	305	306	307	308	309	310	311	312	313	314	315	316	317	318	319	320	321	322	323	324	325	326	327	328	329	330	331	332	333	334	335	336	337	338	339	340	341	342	343	344	345	346	347	348	349	350	351	352	353	354	355	356	357	358	359	360	361	362	363	364	365	366	367	368	369	370	371	372	373	374	375	376	377	378	379	380	381	382	383	384	385	386	387	388	389	390	391	392	393	394	395	396	397	398	399	400	401	402	403	404	405	406	407	408	409	410	411	412	413	414	415	416	417	418	419	420	421	422	423	424	425	426	427	428	429	430	431	432	433	434	435	436	437	438	439	440	441	442	443	444	445	446	447	448	449	450	451	452	453	454	455	456	457	458	459	460	461	462	463	464	465	466	467	468	469	470	471	472	473	474	475	476	477	478	479	480	481	482	483	484	485	486	487	488	489	490	491	492	493	494	495	496	497	498	499	500	501	502	503	504	505	506	507	508	509	510	511	512	513	514	515	516	517	518	519	520	521	522	523	
-----------	---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	--

Db 792 AGGGGACCCGGCTCCACCCACACACATGCGGCCCTAGAGAGCGCAGCCATCTGGAGCA 851
QY 830 AAGAGAAGGATTAACAGAAAGGACACCCCTCTC 861
Db 852 AAGAGAAGGATTAACAGAAAGGACACCCCTCTC 883

Search completed: February 19, 2005, 22:03:58
Job time : 3716.3 secs

Result No.	Score	Query Match	Length	DB	ID	Description	
1	861	100.0	864	11	ADN38809	Cancer/an	
2	861	100.0	1321	6	ABK12137	Human cDN	
3	861	100.0	4839	8	ACC49552	Tumour-as	
4	861	100.0	4839	11	ADP65809	Human STA	
5	861	100.0	4839	11	ADP65729	Human tra	
6	861	100.0	4839	12	ADM67045	Human hom	
7	861	100.0	4839	13	ADR65875	Human pro	
8	861	100.0	4839	13	ADR66778	Human pro	
9	861	100.0	4911	13	ACN40804	Tumour-as	
10	810	94.1	1383	10	ADC37326	Nuclear f	
11	752	87.3	759	10	ADF17545	Human and	
12	752	87.3	759	10	ADH62277	Human PME	
13	752	87.3	759	12	ADO39827	Human PME	
14	752	87.3	1140	6	ABK92120	Prostate	
15	752	87.3	1140	10	AAD60105	Human and	
16	752	87.3	1140	10	ADH62276	Human PME	
17	752	87.3	1140	12	ADO39826	Human PME	
18	752	87.3	1141	10	ADB75588	Prostate	
19	752	87.3	1850	8	ACC49536	Tumour-as	
20	752	87.3	4527	11	ADL83313	Human and	

Qy	661	AGCGGCGGGCGATGGAGGGGGCGCGCCGACCTTAAGGAGGTCAATGGCCACTACCCG	720
Db	961	AGCGGCGGGCGATGGAGGGGGCGCGCCGACCTTAAGGAGGTCAATGGCCACTACCCG	104
Qy	721	GGGTCCTCTTCAGACCCAGCAGAGCAGTGGGCGCCCTCTTGTGTGAGGGGGA	780
Db	1041	GGGTCCTCTTCAGACCCAGCAGAGCAGTGGGCGCCCTCTTGTGTGAGGGGGA	110
Qy	781	CTCCACCCACACACACATCGCGCCCTTAGAGAGCGCGCATCTGGAGCAAGAAGAT	840
Db	1101	CTCCACCCACACACACATCGCGCCCTTAGAGAGCGCGCATCTGGAGCAAGAAGAT	116
Qy	841	AAACAGAAAGACACCCCTCTC	861
Db	1161	AAACAGAAAGACACCCCTCTC	1181
RESULT 7			
ID	ADR65875	ADR65875 standard; DNA; 4839 BP.	
AC	ADR65875;		
D7	02-DEC-2004	(first entry)	
XX	Human prostatic carcinoma derived DNA SEQ ID 71 #1.		
XX	human; cytostatic; diagnosis; prostatic cancer;		
KW	differential expression analysis; ds.		
XX	Homo sapiens.		
XX	WO2004076614-A2.		
PN	10-SEP-2004.		
PD	22-FEB-2004; 2004WO-DE000433.		
PF	27-FEB-2003; 2003DE-01009985.		
PR	14-MAY-2003; 2003DE-01022134.		
XX	(HINZ/) HINZMANN B.		
PA	(DAHL/) DAHL E.		
PA	(ROSE/) ROSENTHAL A.		
PA	(HERM/) HERMANN K.		
PA	(PIL/) PILARSKY C.		
XX	Hinzmann B, Dahl E, Rosenthal A, Hermann K, Pilarsky C, Specht T;		
P1	Schmitt A, Beckmann G, Bruemendorf T, Kluenemann H, Roepeke S;		
P1	Xinzhong L, Staub E,		
XX	WPI; 2004-653386/63.		
DR	New nucleic acids, and encoded proteins, from prostatic cancer tissue,		
XX	useful for diagnosis, treatment and in screening for specific binding		
PT	agents.		
PT	Claim 1; Page 277; 1607pp; German.		
XX	This invention describes novel cytostatic polynucleotide and polypeptide		
CC	sequences which can be used in a method for diagnosing prostatic cancer		
CC	or the risk of developing prostatic cancer. Diagnosis is based on		
CC	determining over transcription or over expression of the sequences in		
CC	prostatic tissue. Screening for inhibitors of the sequences or detection		
CC	substances involves a binding assay, any compounds that bind are		
CC	selected, optionally after deconvolution of mixtures. Detection of a		
CC	predetermined minimum level of the reporter indicates the presence of		
CC	tumour cells. Inhibitors can be chosen from antisense oligonucleotides,		
CC	short-interfering RNA or ribozymes; an organic molecule of molecular		
CC	weight below 5000, preferably 300, that binds to the polypeptide; an		
CC	aptamer against the polypeptide; a (monoclonal) antibody (Ab) against the		
CC	polypeptide, preferably humanised or human; an anti-idiotypic, non-human		

CC	(monoclonal) antibody directed against Ab or any of the above derivatised
CC	with a reporter group, cell toxin, immunostimulatory molecules and/or
CC	radioisotope. The polynucleotides are identified in human prostatic
CC	cancer by differential expression analysis, using DNA microarrays,
CC	between normal and tumorous tissues, with (over)expression being detected
CC	by quantitative PCR. Analysis of prostatic cancer samples showed that
CC	CD24 was upregulated in many of them. Sections of tissue, isolated from
CC	prostatic cancer patients, or subjects at risk, were incubated
CC	sequentially with anti-human CD4 murine monoclonal antibodies;
CC	biotinylated second antibody; streptavidin-conjugated horseradish
CC	peroxidase and then diaminobenzidine as colour former (brown). The
CC	samples were counterstained with hemalum (blue). Malignant cells stained
CC	strongly but non-malignant cells only weakly. In 15 of 63 samples of
CC	adenocarcinoma, membrane and cytoplasmic staining was very strong, and
CC	Lymph node metastases were also stained. ADR65805-ADR6594 represent the
CC	polynucleotide and polypeptide sequences used in the method of the
CC	invention.
XX	
SQ	Sequence 4839 BP; 1103 A; 1313 C; 1290 G; 1133 T; 0 U; 0 Other;
	Query Match 100.0%; Score 861; DB 13; Length 4839;
	Best Local Similarity 100.0%; Pred. No. 0;
	Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
DY	1 ATGACCGCTTGATGGGGGTCAAGACGCCGCCGCCGCCGCCGCAGCCCAATGTC 60
DB	321 ATGACCGCTTGAAGGGGGGTCAAAGACGCCGCCGCCGCCGCCGCAGCCCAATGTC 380
OY	61 TCCTGCACGTGCACTGCAAAACGCTCTTTGTTCCAGAGCATGAGATACA CGSACTGGAG 120
DB	381 TCCTGCACGTGCACTGCAAAACGCTCTTTGTTCCAGAGCATGAGATACA CGSAGCTGGAG 440
OY	121 TTGTGTCAGATCATCATCATGCTGGTGGTAGTAAGTAGTGGTGGTATCAGCTGC 180
DB	441 TTGTGTCAGATCATCATCATGCTGGTGGTAGTAGTAGTAGTAGTGGTGGTATCAGCTGC 500
OY	181 CTGCTGAGCCACTTCAAGAGCTGTCTGCACCGTCTTTCATCAGCCGCGCACAGCTAAGGGCGG 240
DB	501 CTGCTGAGCCACTTCAAGAGCTGTCTGCACCGTCTTTCATCAGCCGCGCACAGCTAAGGGCGG 560
OY	241 AGGAGAGAAGATGCGCTGTCTCTGAGAAGATGCTGTGGGCTGTGGAGAGACAGAGTGTCA 300
DB	561 AGGAGAGAAGATGCGCTGTCTCTGAGAAGATGCTGTGGGCTCTTGGAGAGACAGAGTGTCA 620
OY	301 GGCAACGGAAATCCCAAGAGCGCAGAGTCTAGCGCCCGCCTCGGCCCAACGACCGCCTGGCC 360
DB	621 GGCAACGGAAATCCCAAGAGCGCAGAGTCTAGCGCCCGCCTCGGCCCAACGACCGCCTGGCC 680
OY	361 GTGCGCGCTTTCGCCCAAGCGGAGCGCTTCCACCGCTTCCAGGCCCACTTATCGGTACTGTG 420
DB	681 GTGCGCGCTTTCGCCCAAGCGGAGCGCTTCCACCGCTTCCAGGCCCACTTATCGGTACTGTG 740
OY	421 CAGGACGAGATTCGACCTGGCCACCACCATCTCGGTGTCAAGCGGGAGAGAGGCCCCCAACC 480
DB	741 CAGGACGAGATTCGACCTGGCCACCACCATCTCGGTGTCAAGCGGGAGAGAGGCCCCCAACC 800
OY	481 TACCAAGGAGCCCTTSCAACCTTCAAGCTTTCGGGAGCCCCAGAGCAGAGCTGGAATTGAACCGG 540
DB	801 TACCAAGGAGCCCTTSCAACCTTCAAGCTTTCGGGAGCCCCAGAGCAGAGCTGGAATTGAACCGG 860
OY	541 GAGTCGGTGGCGGCGACCCCAAAACAGAACCATCTTTCGACAGTGA CCTGATGATGATGGCC 600
DB	861 GAGTCGGTGGCGGCGACCCCAAAACAGAACCATCTTTCGACAGTGA CCTGATGATGATGGCC 920
OY	601 AGGCTTGGCGGGCCCCCTTTCGCCACAGATTACTTCGGGGCATCAGGGCCAGATGTGTAAGGC 660
DB	921 AGGCTTGGCGGGCCCCCTTTCGCCACAGATTACTTCGGGGCATCAGGGCCAGATGTGTAAGGC 980
OY	661 AGCGCGGGGCGCATGAGAGGGGCGCGCCCACTTACAGCAGAGGT CATTCGGCCACTACCGG 720
DB	981 AGCGCGGGGCGCATGAGAGGGGCGCGCCCACTTACAGCAGAGGT CATTCGGCCACTACCGG 1040
OY	721 GGGGTCTCTTTCAGACCAAGCAGAGAGCATGTGGCGCGCTCTTGTCTGAGAGGGGACCGG 780

QY	841	AAACGAAAGGACACCCTTCTC	861
Db	1161	AAACAGAAAGGACACCCCTCTC	1181

RESULT 9
ACN40804
ID ACN40804 standard; cDNA; 4911 BP.

AC ACN40804;

DT 18-NOV-2004 (first entry)

DE Tumour-associated antigenic target (TAT) cDNA DNA326860, SEQ ID NO:5823.

KM Tumour-associated antigenic target; TAT; human; overexpression; cancer;
 KM tumour; diagnosis; cell proliferative disorder; breast cancer;
 KM colorectal cancer; lung cancer; ovarian cancer; liver cancer;
 KM central nervous system cancer; bladder cancer; pancreatic cancer;
 KM cervical cancer; melanoma; leukaemia; hybridisation probe;
 KM chromosome identification; chromosome mapping; gene mapping;
 KM gene therapy; cytotoxic; gene; ss.

OS Homo sapiens.

PN WO2004030615-A2.

PD 15-APR-2004.

PF 29-SEP-2003; 2003WO-US028547.
XX

PR 02-OCT-2002; 2002US-0414971P.

PA (GETH) GENENTECH INC.

PI Wu TD, Zhang Z, Zhou Y;

DR WPI; 2004-347921/32.

PT New tumor-associated antigenic target polypeptides and nucleic acids useful in preparing a medicament for treating or detecting a proliferative disorder, e.g. breast, lung, colorectal, ovarian or prostate cancer or tumor.

PS Claim 1; SEQ ID NO 5823; 7273pp; English

CC The invention relates to human tumour-associated antigenic target (TAT)
CC polypeptides, and their related nucleic acids. The TAT polypeptides are
CC overexpressed in cancer tissues compared to normal tissues, and may thus
CC serve as effective targets for the diagnosis and treatment of cancer in
CC mammals. The invention also relates to nucleic acid and polypeptide
CC sequences at least 80% identical to the TAT nucleic acids and
CC polypeptides; expression vectors and host cells comprising a TAT nucleic
CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
CC TAT polypeptide; and methods and compositions for the treatment or
CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
CC antibodies, antigens, binding molecules and compositions are useful
CC for diagnosing or treating a cell proliferative disorder associated with
CC increased TAT expression, particularly cancers such as breast cancer,
CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
CC cancer, pancreatic cancer, cervical cancer, cancers of the central
CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
CC used as hybridisation probes, in chromosome and gene mapping, in
CC chromosome identification and in gene therapy. The present sequence
CC represents a TAT nucleic acid of the invention

SQ Sequence 4911 BP; 1114 A; 1331 C; 1324 G; 1142 T; 0 U; 0 Other;

Query Match	100.0%	Score 861	DB 13	Length 4911
Best Local Similarity	100.0%	Pred. No. 0		
Matches 861	0	Mismatches	0	Gaps 0

[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 18:46:54 ; Search time 159.021 Seconds
(without alignments)
8859.444 Million cell updates/sec

Title: US-09-934-249-3

Perfect score: 861
Sequence: 1 atgacacccctgatg999gtc.....aacagaagacaccctctc 861

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1202784 seqs, 818138359 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :

Issued Patents NA: *
1: /cgm2_6/ptodata/1/ina/5A COMB.seq: *
2: /cgm2_6/ptodata/1/ina/5B COMB.seq: *
3: /cgm2_6/ptodata/1/ina/6A COMB.seq: *
4: /cgm2_6/ptodata/1/ina/6B COMB.seq: *
5: /cgm2_6/ptodata/1/ina/PTUS COMB.seq: *
6: /cgm2_6/ptodata/1/ina/backfile1.seq: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	752	87.3	759	US-09-769-482-2	Sequence 2, Appl1
2	752	87.3	1140	US-09-769-482-1	Sequence 1, Appl1
3	30	3.5	142783	US-09-949-016-15127	Sequence 15127, A
4	29	3.4	3430	US-09-949-016-1263	Sequence 1263, Ap
5	29	3.4	9406	US-09-949-016-13005	Sequence 13005, A
6	29	3.4	34230	US-09-949-016-12052	Sequence 12052, A
7	29	3.4	128470	US-09-949-016-13765	Sequence 13765, A
8	26	3.0	198942	US-09-949-016-13209	Sequence 13209, A
9	26	3.0	254405	US-09-949-016-14381	Sequence 14381, A
10	24	2.8	431	US-09-513-9999C-9263	Sequence 9263, Ap
11	24	2.8	119762	US-09-949-016-17313	Sequence 17313, A
12	23	2.7	377	US-08-332-766A-1	Sequence 1, Appl1
13	23	2.7	1212	US-09-248-796A-6566	Sequence 6566, Ap
14	23	2.7	10304	US-09-627-465B-1	Sequence 1, Appl1
15	23	2.7	55195	US-09-949-016-15854	Sequence 15854, A
16	22	2.6	22	US-09-769-482-8	Sequence 8, Appl1
17	22	2.6	209	US-09-513-9999C-14394	Sequence 14394, A
18	22	2.6	39154	US-09-949-016-12384	Sequence 12384, A
19	22	2.6	39154	US-09-949-016-12801	Sequence 12801, A
20	22	2.6	39443	US-09-949-016-14326	Sequence 14326, A
21	22	2.6	39443	US-09-949-016-14327	Sequence 14327, A
22	22	2.6	70770	US-09-949-016-16938	Sequence 16938, A
23	22	2.6	94019	US-09-949-016-13203	Sequence 13203, A
24	21	2.4	633	US-08-234-783-1	Sequence 1, Appl1
25	21	2.4	633	US-08-456-907-1	Sequence 1, Appl1
26	21	2.4	633	PCT-US95-05523-1	Sequence 1, Appl1
27	21	2.4	1327	US-08-165-315D-3	Sequence 3, Appl1

28	21	2.4	1661	US-09-436-521A-1	Sequence 1, Appl1
29	21	2.4	4659	US-08-264-578-10	Sequence 10, Appl1
30	21	2.4	4659	US-08-217-704C-9	Sequence 9, Appl1
31	21	2.4	4659	US-08-164-487A-1	Sequence 1, Appl1
32	21	2.4	7710	US-09-949-016-738	Sequence 738, Ap
33	21	2.4	8147	US-09-514-247A-9	Sequence 9, Appl1
34	21	2.4	8242	US-09-949-016-4620	Sequence 4620, Ap
35	21	2.4	8252	US-08-046-585-15	Sequence 15, Appl1
36	21	2.4	8252	US-08-393-703-15	Sequence 15, Appl1
37	21	2.4	8252	PCT-US93-11721-15	Sequence 15, Appl1
38	21	2.4	21170	US-09-949-016-12460	Sequence 12460, A
39	21	2.4	27630	US-09-949-016-16362	Sequence 16362, A
40	21	2.4	31391	US-09-949-016-14319	Sequence 14319, A
41	21	2.4	1664976	US-08-916-421B-1	Sequence 1, Appl1
42	21	2.4	1664976	US-09-692-570-1	Sequence 1, Appl1
43	20	2.3	20	US-09-769-482-9	Sequence 9, Appl1
44	20	2.3	50	US-08-753-247-22	Sequence 22, Appl1
45	20	2.3	51	US-08-753-247-23	Sequence 23, Appl1

ALIGNMENTS

```
RESULT 1
US-09-769-482-2
; Sequence 2, Application US/09769482
; Patent No. 6566130
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; TITLE OF INVENTION: POYNUCLEOTIDE ARRAY
; FILE REFERENCE: 04995, 0057-00000
; CURRENT APPLICATION NUMBER: US/09/769, 482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178, 772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179, 045
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-769-482-2

Query Match      87.3%; Score 752; DB 4; Length 759;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 CGAGCTGAGATTGTTTCAGATCATCATCTGCTGCTGATGATGATGATGATG 169
Db 5 CGAGCTGAGATTGTTTCAGATCATCATCTGCTGCTGATGATGATGATGATG 64

QY 170 TGATCAGTGTCTGCTGATGATGATGATGATGATGATGATGATGATGATG 229
Db 65 TGATCAGTGTCTGCTGATGATGATGATGATGATGATGATGATGATGATG 124

QY 230 GCCAGGGGGGGAGAGAGATGCTGCTGCTGATGATGATGATGATGATGATG 289
Db 125 GCCAGGGGGGGAGAGAGATGCTGCTGCTGATGATGATGATGATGATGATG 184

QY 290 GCACAGTGTCAAGGACGATCCAGAGCGGAGGCTTCAAGCCCTCGCCACCG 349
Db 185 GCACAGTGTCAAGGACGATCCAGAGCGGAGGCTTCAAGCCCTCGCCACCG 244

QY 350 ACCGCTGCGCGCGCGCGCGCTTGGCCGAGGAGCGCTTCAAGCCCTCG 409
Db 245 ACCGCTGCGCGCGCGCGCGCTTGGCCGAGGAGCGCTTCAAGCCCTCG 304
```


TITLE OF INVENTION: SIMPLE TANDEM REPEATS
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN DARBY & CUSHMAN, L.L.P.
STREET: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D. C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/332,766A
FILING DATE: 01-NOV-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9326052.9
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: BIRD, Donald J.
REGISTRATION NUMBER: 25,323
REFERENCE/DOCKET NUMBER: 217211/M94/0434/GB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 377 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-332-766A-1

Query Match 2.7%; Score 23; DB 2; Length 377;
Best Local Similarity 100.0%; Pred. No. 0.68;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGTGTGATGATGTGATGTG 165
DB 123 TGGTGTGATGATGTGATGTG 145

RESULT 13
US-09-248-796A-6566/C
Sequence 6566, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 6566
LENGTH: 1212
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-6566

Query Match 2.7%; Score 23; DB 4; Length 1212;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 142 TGGTGTGATGATGTGATGTG 164
DB 342 TGGTGTGATGATGTGATGTG 320

RESULT 14
US-09-627-465B-1
Sequence 1, Application US/09627465B
Patent No. 6737519
GENERAL INFORMATION:
APPLICANT: KEITH, TIM
APPLICANT: LITTLE, RANDALL D.
APPLICANT: BERDEWEGH, PAUL VAN
APPLICANT: DUPUIS, JOSEF
APPLICANT: DEL MASTRO, RICHARD L.
APPLICANT: SIMON, JASON
APPLICANT: ALLEN, KRISTINA
APPLICANT: PANDIT, SUNIL
TITLE OF INVENTION: NOVEL HUMAN GENES RELATING TO RESPIRATORY DISEASES AND OBESITY
FILE REFERENCE: 2976-4037
CURRENT APPLICATION NUMBER: US/09/627,465B
CURRENT FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: 60/211,749
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: 60/146,336
PRIOR FILING DATE: 1999-07-30
NUMBER OF SEQ ID NOS: 51
SOFTWARE: Patentin Ver 2.1
SEQ ID NO 1
LENGTH: 10304
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: modified_base
LOCATION: (267)
OTHER INFORMATION: a, t, c or g
US-09-627-465B-1

Query Match 2.7%; Score 23; DB 4; Length 10304;
Best Local Similarity 100.0%; Pred. No. 0.61;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 143 TGGTGTGATGATGTGATGTG 165
DB 10242 TGGTGTGATGATGTGATGTG 10264

RESULT 15
US-09-949-016-15854/C
Sequence 15854, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: C1001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15854
LENGTH: 55195
TYPE: DNA
ORGANISM: Human
US-09-949-016-15854

Query Match 2.7%; Score 23; DB 4; Length 55195;

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 19, 2005, 19:27:04 ; Search time 483.77 Seconds
(without alignments)
10519.334 Million cell updates/sec

Title: US-09-934-249-3
Perfect score: 861
Sequence: 1 atgcaccgcctgctgagggggtc.....aacagaagacaccccttc 861

Scoring table:
OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 5384158 seqs, 2955248155 residues

Word size : 0

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications NA:*
1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
4: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/2/pubpna/US09A_PUBCOMB.seq:*
10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/2/pubpna/US09C_NEW_PUB.seq:*
13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:*
14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:*
15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:*
16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
17: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:*
19: /cgn2_6/ptodata/2/pubpna/US10F_NEW_PUB.seq:*
20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	861	100.0	861	9 US-09-934-249-3	Sequence 3, Appl1
2	861	100.0	864	17 US-10-295-027-127	Sequence 127, App
3	861	100.0	1321	9 US-09-934-249-1	Sequence 1, Appl1
4	861	100.0	4839	15 US-10-241-220-119	Sequence 119, App
5	861	100.0	4839	16 US-10-269-909-84	Sequence 84, Appl
6	861	100.0	4839	16 US-10-269-909-85	Sequence 85, Appl
7	861	100.0	4839	18 US-10-872-972-119	Sequence 119, App
8	861	100.0	4839	18 US-10-872-972-119	Sequence 119, App
9	752	87.3	759	16 US-10-390-045-2	Sequence 2, Appl1
10	752	87.3	759	17 US-10-434-479-2	Sequence 2, Appl1
11	752	87.3	1140	16 US-10-390-045-1	Sequence 1, Appl1

12	752	87.3	1140	17	US-10-434-479-1	Sequence 1, Appl1
13	752	87.3	1141	15	US-10-205-823-412	Sequence 412, App
14	752	87.3	1141	15	US-10-301-822-208	Sequence 208, App
15	752	87.3	1850	15	US-10-241-220-44	Sequence 44, Appl
16	752	87.3	1850	18	US-10-872-972-44	Sequence 44, Appl
17	752	87.3	1850	18	US-10-872-972-44	Sequence 44, Appl
18	752	87.3	1850	18	US-10-872-972-44	Sequence 44, Appl
19	752	87.3	4527	18	US-09-821-812-2	Sequence 2, Appl1
20	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
21	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
22	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
23	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
24	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
25	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
26	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
27	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
28	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
29	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
30	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
31	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
32	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
33	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
34	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
35	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
36	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
37	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
38	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
39	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
40	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
41	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
42	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
43	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
44	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1
45	752	87.3	4527	18	US-10-849-635-2	Sequence 2, Appl1

ALIGNMENTS

RESULT 1
US-09-934-249-3 Application US/09934249
Sequence 3, Appl1
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landschulz, Katherine T.
APPLICANT: Turti, Thomas G.
APPLICANT: Thompson, John F.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: P0738/7001/ERF/KA
CURRENT APPLICATION NUMBER: US/09/934,249
CURRENT FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ For Windows Version 3.0
SEQ ID NO 3
LENGTH: 861
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1) ... (861)
US-09-934-249-3
Query Match 100.0%; Score 861; DB 9; Length 861;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 ATGCACCGCTTGTATGGGGTCAACAGCAGCCGCGCCGCGCGGAGCCCATGTC 60
|||||

[illegible]

```

1  APPLICANT: Eos Biotechnology, Inc.
2  TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
3  TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
4  FILE REFERENCE: 018501-012500US
5  CURRENT APPLICATION NUMBER: US/10/295,027
6  CURRENT FILING DATE: 2002-11-13
7  PRIOR APPLICATION NUMBER: US 09/663,733
8  PRIOR FILING DATE: 2000-09-15
9  PRIOR APPLICATION NUMBER: US 60/350,666
10 PRIOR FILING DATE: 2001-11-13
11 PRIOR APPLICATION NUMBER: US 60/335,394
12 PRIOR FILING DATE: 2001-11-15
13 PRIOR APPLICATION NUMBER: US 60/332,464
14 PRIOR FILING DATE: 2001-11-21
15 PRIOR APPLICATION NUMBER: US 60/334,393
16 PRIOR FILING DATE: 2001-11-29
17 PRIOR APPLICATION NUMBER: US 60/340,376
18 PRIOR FILING DATE: 2001-12-14
19 PRIOR APPLICATION NUMBER: US 60/347,211
20 PRIOR FILING DATE: 2002-01-08
21 PRIOR APPLICATION NUMBER: US 60/347,349
22 PRIOR FILING DATE: 2002-01-10
23 PRIOR APPLICATION NUMBER: US 60/355,250
24 PRIOR FILING DATE: 2002-02-08
25 PRIOR APPLICATION NUMBER: US 60/356,714
26 PRIOR FILING DATE: 2002-02-13
27 Remaining Prior Application data removed - See File Wrapper or PALM.
28 NUMBER OF SEQ ID NOS: 1386
29 SOFTWARE: PatentIn Ver. 2.1
30 SEQ ID NO 127
31 LENGTH: 864
32 TYPE: DNA
33 ORGANISM: Homo sapiens
34 US-10-295-027-127

```

Query Match	100.0%;	Score 861;	DB 17;	Length 864;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 861; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

Qy	1	ATGCAACCGGTTGATGGGGGTCAACAGCACCGGCGCGCGCGCGCGGGAGACCCCAATGTC	60
Db	1	ATGCAACCGTTGATGGGGGTCAACAGCACCGGCGCGCGCGCGCGGGAGACCCCAATGTC	60
Qy	61	TCCTGCAAGTGCACTGCAAAAGCGCTCTTGTGTTCCAGAGCATGAGAGATACAGGAAGTTGAG	120
Db	61	TCCTGCAAGTGCACTGCAAAAGCGCTCTTGTGTTCCAGAGCATGAGAGATACAGGAAGTTGAG	120
Qy	121	TTTGTTCAGATCATCATATATGCTGTGTGTGTATGTATGTATGTATGATGATCACTGTC	180
Db	121	TTTGTTCAGATCATCATCATATGCTGTGTGTGTATGTATGTATGTATGATGATCACTGTC	180
Qy	181	CTGCTGAGCCACTACAAAGCTGTGCAACGGATCCCTTCACTCAACCGGCAACGCCAAGGGCGG	240
Db	181	CTGCTGAGCCACTACAAAGCTGTGCAACGGATCCCTTCACTCAACCGGCAACGCCAAGGGCGG	240
Qy	241	AGGAGAGAGATGCGCCCTGTCTCTCAGAAAGATGCGCTGTGACCCTTGAGAGACAGTGTCA	300
Db	241	AGGAGAGAGATGCGCCCTGTCTCTCAGAAAGATGCGCTGTGACCCTTGAGAGACAGTGTCA	300
Qy	301	GGCAACGGAAATCCCAAGACCGCAGGTCTAGCGCCCGGCTTGAGCCACCGAACCGGCTTGCC	360
Db	301	GGCAACGGAAATCCCAAGACCGCAGGTCTAGCGCCCGGCTTGAGCCACCGAACCGGCTTGCC	360
Qy	361	GTGCGCGCCCTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCAGACCCACTTATCCGTACTG	420
Db	361	GTGCGCGCCCTTCGCGCCAGCGGAGCGCTTCCACCGCTTCCAGACCCACTTATCCGTACTG	420
Qy	421	CAGCAGCAGATTCGACTGTGCCACCCACCATCTGCTGTAGACGGGAGAGAGCCGCCACCC	480
Db	421	CAGCAGCAGATTCGACTGTGCCACCCACCATCTGCTGTAGACGGGAGAGAGCCGCCACCC	480
Qy	481	TACCAAGGGCCCTGCACCCCTTCAGCTTCGGGACCCCGAGCAGCAGCTGGAATTGAACCGG	540
Db	481	TACCAAGGGCCCTGCACCCCTTCAGCTTCGGGACCCCGAGCAGCAGCTGGAATTGAACCGG	540

Db 481 TACCAGGCGCCCTTCAGCCTTCAGGAGCCCGAGCAGCTGGAACCTGAACCGG 540
Qy 541 GAGTCGGGCGCGACCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGATGATGAGCC 600
Db 541 GAGTCGGGCGCGACCCCGCAACAGAACCATCTTTCAGAGTGAAGCTGATGATGAGCC 600
Qy 601 AGGCTGGGCGGCGCCCTTCGAGGAGTGAAGCTGAGGAGTGAAGGAGTGAAGGAG 660
Db 601 AGGCTGGGCGGCGCCCTTCGAGGAGTGAAGCTGAGGAGTGAAGGAGTGAAGGAG 660
Qy 661 AGGCGGGGCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 661 AGGCGGGGCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Qy 721 GGGTCTCTCTTCAGAGCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Db 721 GGGTCTCTCTTCAGAGCAGAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 780
Qy 781 CTCACACACACACATCGGCGCCCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 781 CTCACACACACACATCGGCGCCCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Qy 841 AAACAGAAAGAGACCTCTTC 861
Db 841 AAACAGAAAGAGACCTCTTC 861

RESULT 3

US-09-934-249-1
Sequence 1, Application US/09934249
Patent No. US20020115081A1
GENERAL INFORMATION:
APPLICANT: Lee, Richard T.
APPLICANT: Landeshulz, Katherine T.
APPLICANT: Turf, Thomas G.
APPLICANT: Thompson, John P.
APPLICANT: Kennedy, Scott P.
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF
FILE REFERENCE: P0738/7001/ERP/KA
CURRENT APPLICATION NUMBER: US/09/934,249
PRIOR FILING DATE: 2001-08-21
PRIOR APPLICATION NUMBER: US 60/227,159
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 1
LENGTH: 1321
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (413)...(1273)
US-09-934-249-1

Query Match 100.0%; Score 861; DB 9; Length 1321;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGCACCGCTTGAAGGAGTCAACAGACCGCGCCCGCCCGCGCGGAGCCCAATGTC 60
Db 413 ATGCACCGCTTGAAGGAGTCAACAGACCGCGCCCGCCCGCGGAGCCCAATGTC 472
Qy 61 TCCGTCAGTCGACATGCAAAACGCTCTTTGTCAGAGCATGAGATCAGAGAGTGAAG 120
Db 473 TCCGTCAGTCGACATGCAAAACGCTCTTTGTCAGAGCATGAGATCAGAGAGTGAAG 532
Qy 121 TTGTCAGATCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
Db 533 TTGTCAGATCATCATCATGATGATGATGATGATGATGATGATGATGATGATGATGAT 592
Qy 181 CTGCTGAGCAGTCAAGAGTGTGTCAGGAGTCTTCATCAGCGGCGCAGCGAGGAGCG 240
Db 181 CTGCTGAGCAGTCAAGAGTGTGTCAGGAGTCTTCATCAGCGGCGCAGCGAGGAGCG 240

Db 593 CTGCTGAGCAGTCAAGAGTGTGTCAGGAGTCTTCATCAGCGGCGCAGCGAGGAGCG 652
Qy 241 AGGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
Db 653 AGGAGAGAGATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 712
Qy 301 GGCAGAGAAATCCAGAGCGCAGAGTCTACGCGCCGCTCGGCGCAGCGAGCGGAGGAG 360
Db 713 GGCAGAGAAATCCAGAGCGCAGAGTCTACGCGCCGCTCGGCGCAGCGAGCGGAGGAG 772
Qy 361 GTGCGCGCTTCGCGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 420
Db 773 GTGCGCGCTTCGCGCAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 832
Qy 421 CAGACAGATTCAGACTGTCACACCATCTGCTGTCAGAGGAGGAGGAGGAGGAGGAG 480
Db 833 CAGACAGATTCAGACTGTCACACCATCTGCTGTCAGAGGAGGAGGAGGAGGAGGAG 892
Qy 481 TACCAGGCGCCCTTCAGACCTTCAGCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAG 540
Db 893 TACCAGGCGCCCTTCAGACCTTCAGCTTCGAGGAGGAGGAGGAGGAGGAGGAGGAG 952
Qy 541 GAGTCGGTGGCGGACCCCGCAACAGAACCATCTTTCAGAGTGAAGTGAAGTGAAG 600
Db 953 GAGTCGGTGGCGGACCCCGCAACAGAACCATCTTTCAGAGTGAAGTGAAGTGAAG 1012
Qy 601 AGGCTGGGCGGCGCCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 660
Db 1013 AGGCTGGGCGGCGCCCTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1072
Qy 661 AGGCGGGGCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 720
Db 1073 AGGCGGGGCGGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1132
Qy 721 GGGTCTCTCTTCAGAGCAGAGAGAGTGGGCGCGCTTCCTGTCGAGGAGGAGGAG 780
Db 1133 GGGTCTCTCTTCAGAGCAGAGAGAGTGGGCGCGCTTCCTGTCGAGGAGGAGGAG 1192
Qy 781 CTCACACACACACATCGGCGCCCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 840
Db 1193 CTCACACACACACATCGGCGCCCTTCAGAGGAGGAGGAGGAGGAGGAGGAGGAG 1252
Qy 841 AAACAGAAAGAGACCTCTTC 861
Db 1253 AAACAGAAAGAGACCTCTTC 1273

RESULT 4

US-10-241-220-119
Sequence 119, Application US/10241220
Publication No. US20030148408A1
GENERAL INFORMATION:
APPLICANT: Frantz, Gretchen
APPLICANT: Hillan, Kenneth J.
APPLICANT: Phillips, Heidi
APPLICANT: Polakis, Paul
APPLICANT: Spencer, Susan
APPLICANT: Williams, P. Mickey
APPLICANT: Wu, Thomas
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
FILE REFERENCE: P5010R1-US
CURRENT APPLICATION NUMBER: US/10/241,220
PRIOR FILING DATE: 2002-12-13
NUMBER OF SEQ ID NOS: 120
SEQ ID NO 119
LENGTH: 4839
TYPE: DNA
ORGANISM: Homo Sapiens
US-10-241-220-119

Query Match 100.0%; Score 861; DB 15; Length 4839;


```

Db 561 AGGAGGAAATATCCCTGCTCTGAGAGAGATGCTTGCCCTCGAGAGACAGATGCA 620
Qy 301 GGCAAGGAATCCCAAGAGCCGAGATCTAGGCCCCCTCGGCGCAAGAGCCGCTGCGC 360
Db 621 GGCAAGGAATCCCAAGAGCCGAGATCTAGGCCCCCTCGGCGCAAGAGCCGCTGCGC 680
Qy 361 GTGCGCCCTTCCGCGAGAGAGGCTTCAAGGCTTCCAGCCCACTATCCGTAAGTCTG 420
Db 681 GTGCGCCCTTCCGCGAGAGAGGCTTCAAGGCTTCCAGCCCACTATCCGTAAGTCTG 740
Qy 421 CAGACAGATGCACTGCAAGCCATCTGCTGTCAGAGGAGAGAGAGAGAGAGAGAGAG 480
Db 741 CAGACAGATGCACTGCAAGCCATCTGCTGTCAGAGGAGAGAGAGAGAGAGAGAGAG 800
Qy 481 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 801 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Qy 541 GAGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 861 GAGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
Qy 601 AGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 921 AGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Qy 661 AGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 981 AGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Qy 721 GGGTCCTCTTCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 1041 GGGTCCTCTTCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
Qy 781 CTCACACACACACACATGCGCGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 840
Db 1101 CTCACACACACACACATGCGCGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1160
Qy 841 AAACAGAAAGAGACACCTCTC 861
Db 1161 AAACAGAAAGAGACACCTCTC 1181

```

RESULT 8

```

US-10-872-991-119
; Sequence 119, Application US/10872991
; Publication No. US20040242860A1
; GENERAL INFORMATION:
; APPLICANT: Frantz, Gretchen
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Phillips, Heidi
; APPLICANT: Polakis, Paul
; APPLICANT: Spencer, Susan
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wu, Thomas
; APPLICANT: Zhang, Zhen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; FILE REFERENCE: P5010R1-US
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: US/10/241,220
; PRIORITY FILING DATE: 2002-09-11
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO 119
; LENGTH: 4839
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-10-872-991-119

```

```

Query Match 100.0%; Score 861; DB 18; Length 4839;
Best Local Similarity 100.0%; Pred. No. 0;

```

```

Matches 861; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 ATGCACCGCTTGTATGGGGTCAACAGACCGCGCGCGCGCGAGCCCAATGTC 60
Db 321 ATGCACCGCTTGTATGGGGTCAACAGACCGCGCGCGCGCGAGCCCAATGTC 380
Qy 61 TTCGCAAGAGCAATGCAAAAGCTCTTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 120
Db 381 TTCGCAAGAGCAATGCAAAAGCTCTTGTTCAGAGAGAGAGAGAGAGAGAGAGAGAG 440
Qy 121 TTTGTTCAGATCATCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 180
Db 441 TTTGTTCAGATCATCATATGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTT 500
Qy 181 CTGCTGAGCCATCAAGAGTGTGCAAGGCTTCAATCAGCCGAGAGAGAGAGAGAGAGAG 240
Db 501 CTGCTGAGCCATCAAGAGTGTGCAAGGCTTCAATCAGCCGAGAGAGAGAGAGAGAGAG 560
Qy 241 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Db 561 AGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 620
Qy 301 GGCAACGAATCCCAAGAGCCGAGTCTAGCCCGCGCTCGGCGCAAGAGAGAGAGAGAG 360
Db 621 GGCAACGAATCCCAAGAGCCGAGTCTAGCCCGCGCTCGGCGCAAGAGAGAGAGAGAG 680
Qy 361 GTGCGGCGCTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
Db 681 GTGCGGCGCTTGGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 740
Qy 421 CAGACAGATGACCTGCAACCAATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 480
Db 741 CAGACAGATGACCTGCAACCAATCTGCTGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 800
Qy 481 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
Db 801 TACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 860
Qy 541 GAGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Db 861 GAGTCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 920
Qy 601 AGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Db 921 AGGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 980
Qy 661 AGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 720
Db 981 AGGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1040
Qy 721 GGGTCCTCTTCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 780
Db 1041 GGGTCCTCTTCCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1100
Qy 781 CTCACACACACACACATGCGCGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 840
Db 1101 CTCACACACACACACATGCGCGCCCTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 1160
Qy 841 AAACAGAAAGAGACACCTCTC 861
Db 1161 AAACAGAAAGAGACACCTCTC 1181

```

RESULT 9

```

US-10-390-045-2
; Sequence 2, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOU, JUDD W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED

```

```

1 TITLE OF INVENTION: POYNCLEOTIDE ARRAY
2
3 FILE REFERENCE: 04995, 0057-00000
4
5 CURRENT APPLICATION NUMBER: US/10/390, 045
6
7 CURRENT FILING DATE: 2003-03-18
8
9 PRIOR APPLICATION NUMBER: US/09/769, 482
10
11 PRIOR FILING DATE: 2001-01-26
12
13 PRIOR APPLICATION NUMBER: 60/178, 772
14
15 PRIOR FILING DATE: 2000-01-28
16
17 PRIOR APPLICATION NUMBER: 60/179, 045
18
19 PRIOR FILING DATE: 2000-01-31
20
21 NUMBER OF SEQ ID NOS: 67
22
23 SOFTWARE: PatentIn Ver. 2.1
24
25 SEQ ID NO 2
26
27 LENGTH: 759
28
29 TYPE: DNA
30
31 ORGANISM: Homo sapiens
32
33 US-10-390-045-2

```

Query Match	87.3%	Score 752	DB 16	Length 759
Best Local Similarity	100.0%	Pred. No. 0		
Matches 752; Conservative	0	Mismatches	0	Indels 0
				Gaps 0

[illegible]

```

RESULT 10
US-10-434-479-2
; Sequence 2, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOUL, JUDD W.
; APPLICANT: XU, LINDA L.
; TITLE OR INVENTION: ANDROGEN-REGULATED PMEPA1 GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; CURRENT FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 81
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 759
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-434-479-2

```

Query Match	87.3%;	Score 752;	DB 17;	Length 759;
Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 752; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

OY	110	CGAGCGTGAAGTTGTTTCAAGTATCATTCATCGTGTGTGTATGATATGTGTATG	165
Db	5	CGAGCGTGAAGTTGTTTCAAGTATCATTCATCGTGTGTGTATGATATGTGTGTGTG	64
OY	170	TGATCAGGTGCTCTGATGCGCATCAAGAAGCTGTGTGACGGTCTTTCATCAGCGGCACA	229
Db	65	TGATCAGGTGCTCTGATGCGCATCAAGAAGCTGTGTGACGGTCTTTCATCAGCGGCACA	124
OY	230	GCCAGGGGCGAGGAGAGAAAGATGCGCTGTCTTCAGAGAGATGCTGTGGCCTTCGAGAGA	289
Db	125	GCCAGGGGCGAGGAGAGAAAGATGCGCTGTCTTCAGAGAGATGCTGTGGCCTTCGAGAGA	184
OY	290	GCAAGGTGTAGGCGAAGGAATCCCAAGCGCGCAGGTCTAAGCCCGCTTGTGGCCACCG	349
Db	185	GCAAGGTGTAGGCGAAGGAATCCCAAGCGCGCAGGTCTAAGCCCGCTTGTGGCCACCG	244
OY	350	ACGCGCTGGCGGTGCGCGCCCTTGCGCGAGGGAGCGGCTTCACCGGCTTCAGGCCACCT	409
Db	245	ACGCGCTGGCGGTGCGCGCCCTTGCGCGAGGGAGCGGCTTCACCGGCTTCAGGCCACCT	304
OY	410	ATTCGTACTGTGACAGCAGATGCACTGTGCACCCACCATCTGTGCTGTACAGCGGGAGG	469
Db	305	ATTCGTACTGTGACAGCAGATGCACTGTGCACCCACCATCTGTGCTGTACAGCGGGAGG	364
OY	470	AGCCCCACCTTCACAGGGGCCCTTGTGCACCTTCCAGCTTTCGGAGCCCGAGCAGCATGTG	529
Db	365	AGCCCCACCTTCACAGGGGCCCTTGTGCACCTTCCAGCTTTCGGAGCCCGAGCAGCATGTG	424
OY	530	AACCTGAACCGGGAAGTCGGTGTGGGCAACCCCAACAGAACCATCTTTCGACAGTACCTGA	589
Db	425	AACCTGAACCGGGAAGTCGGTGTGGGCAACCCCAACAGAACCATCTTTCGACAGTACCTGA	484
OY	590	TGATAGTGTCCAGGCTGGGCGGCCCTTGCCCGCCAGCAGTAACCTTCGGGCAATCAGCGCA	649
Db	485	TGATAGTGTCCAGGCTGGGCGGCCCTTGCCCGCCAGCAGTAACCTTCGGGCAATCAGCGCA	544
OY	650	CGTGTCTACGCGCAGGGGGGGCGCATTGAGAGGGGCGCGGCCCATCTTAAGCAGGTCTATGG	709
Db	545	CGTGTCTACGCGCAGGGGGGGCGCATTGAGAGGGGCGCGGCCCATCTTAAGCAGGTCTATGG	604

QY 710 GCCACTACCCGGGGTCTCTTCCAGACACAGAGAGATGGGCGCCCTCTTGTCTGG 769
DB 605 GCCACTACCCGGGGTCTCTTCCAGACACAGAGAGATGGGCGCCCTCTTGTCTGG 664
QY 770 AGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGGCGACCATCTGGAGCA 829
DB 665 AGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGGCGACCATCTGGAGCA 724
QY 830 AAGAGAGATTAACAGAAAGACACCCCTCTC 861
DB 725 AAGAGAGATTAACAGAAAGACACCCCTCTC 756

RESULT 11

US-10-390-045-1
; Sequence 1, Application US/10390045
; Publication No. US20030170713A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOULI, JUDDA W.
; APPLICANT: XU, LINDA L.
; APPLICANT: SEGAWA, TAKEHIKO
; TITLE OF INVENTION: PROSTATE-SPECIFIC ANDROGEN-SIGNALING-ASSOCIATED
; FILE REFERENCE: 04995.0057-00000
; CURRENT APPLICATION NUMBER: US/10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: US/09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(850)
US-10-390-045-1

Query Match 87.3%; Score 752; DB 16; Length 1140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 CGGAGCTGAGATTGTTCAATCATCATCATCTGCTGATGATGATGATGATGATG 169
DB 99 CGGAGCTGAGATTGTTCAATCATCATCATCTGCTGATGATGATGATGATGATG 158
QY 170 TGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 229
DB 159 TGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 218
QY 230 GCCAGGGGCGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 289
DB 219 GCCAGGGGCGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 278
QY 290 GCACAGTGTCAAGGACGAAATCCCAAGCCGCGAGGTCTACGCCGCCCTCGGCCAC 349
DB 279 GCACAGTGTCAAGGACGAAATCCCAAGCCGCGAGGTCTACGCCGCCCTCGGCCAC 338
QY 350 ACCGCTGCGCGGCTGCGCGCTGCGCGCGCGAGAGGCGCTTCAACCGCTTCAACCCACT 409
DB 339 ACCGCTGCGCGGCTGCGCGCTTCCGCGCGAGGCGCTTCAACCGCTTCAACCCACT 398
QY 410 ATCCGTAATCTGACAGCAGATGCACTGCGACCCACCATCTGCTGTGAGAAGGAGAG 469
DB 399 ATCCGTAATCTGACAGCAGATGCACTGCGACCCACCATCTGCTGTGAGAAGGAGAG 458

QY 470 AGCCCCACCCCTTACAGAGGCGCCCTGACACCTTCCAGCTTCCGAGACCCCGAGACAGCTGG 529
DB 459 AGCCCCACCCCTTACAGAGGCGCCCTGACACCTTCCAGCTTCCGAGACCCCGAGAGAGCTGG 518
QY 530 AACTGAACCCGGGAGTCCGTGCGGACACCCCAACAGAACCATCTTGAAGTGAAGCTGA 589
DB 519 AACTGAACCCGGGAGTCCGTGCGGACACCCCAACAGAACCATCTTGAAGTGAAGCTGA 578
QY 590 TGGATAGTGCAGAGCTGGGGGCGCCCTGCGCCCTCCAGCACTTAACCTGGGAGTACAGGCGCA 649
DB 579 TGGATAGTGCAGAGCTGGGGGCGCCCTGCGCCCTCCAGCACTTAACCTGGGAGTACAGGCGCA 638
QY 650 CGTGTACAGCAGAGCGGCGGCGATGAGAGGCGCGCCCACTTACAGGAGATATCG 709
DB 639 CGTGTACAGCAGAGCGGCGGCGATGAGAGGCGCGCCCACTTACAGGAGATATCG 698
QY 710 GCCACTACCCGGGGTCTCTTCCAGACACAGACAGATGAGGAGCGCTCTTGTCTGG 769
DB 699 GCCACTACCCGGGGTCTCTTCCAGACACAGACAGATGAGGAGCGCTCTTGTCTGG 758
QY 770 AGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGGCGGACCATCTGGAGCA 829
DB 759 AGGGGACCCGGGCTCCACACACACATCGCGCCCTTAGAGAGGCGGACCATCTGGAGCA 818
QY 830 AAGAGAGATTAACAGAAAGACACCCCTCTC 861
DB 819 AAGAGAGATTAACAGAAAGACACCCCTCTC 850

RESULT 12

US-10-434-479-1
; Sequence 1, Application US/10434479
; Publication No. US20040092469A1
; GENERAL INFORMATION:
; APPLICANT: SRIVASTAVA, SHIV
; APPLICANT: MOULI, JUDDA W.
; APPLICANT: XU, LINDA L.
; TITLE OF INVENTION: ANDROGEN-REGULATED PHEPAl GENE AND POLYPEPTIDES
; FILE REFERENCE: 04995.0057-02000
; CURRENT APPLICATION NUMBER: US/10/434,479
; PRIOR FILING DATE: 2003-05-09
; PRIOR APPLICATION NUMBER: 10/390,045
; PRIOR FILING DATE: 2003-03-18
; PRIOR APPLICATION NUMBER: 09/769,482
; PRIOR FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: 60/178,772
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/179,045
; PRIOR FILING DATE: 2000-01-31
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1140
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (95)..(850)
US-10-434-479-1

Query Match 87.3%; Score 752; DB 17; Length 1140;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 110 CGGAGCTGAGATTGTTCAATCATCATCATCTGCTGATGATGATGATGATGATG 169
DB 99 CGGAGCTGAGATTGTTCAATCATCATCATCTGCTGATGATGATGATGATGATG 158
QY 170 TGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 229
DB 159 TGATCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 218
QY 230 GCCAGGGGCGGAGAGAGAGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 289


```
Db 219 GCCAGGGGGGAGAGAGATGCTCTCTCAGAGAGATGCTGTGGCCCTCGAGA 278
Qy 290 GCACAGTGTCAAGGAGAAATCCCAAGCCGAGGTCTAGCCGCCCTCGGCCACCG 349
Db 279 GCACAGTGTCAAGGAGAAATCCCAAGCCGAGGTCTAGCCGCCCTCGGCCACCG 338
Qy 350 ACCGCTGAGCGGTGCGCCCTTCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCACT 409
Db 339 ACCGCTGAGCGGTGCGCCCTTCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCACT 398
Qy 410 ATCCGTAAGCTGACAGAGATGCACTGCACTCCATCTGCTGTGAGACGGGAGG 469
Db 399 ATCCGTAAGCTGACAGAGATGCACTGCACTCCATCTGCTGTGAGACGGGAGG 458
Qy 470 AGCCCCCACTTACAGAGGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCACTG 529
Db 459 AGCCCCCACTTACAGAGGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCACTG 518
Qy 530 AACTGAACCGGAGTGTGAGGCGCACTCCCAAGCAATCTTGAAGTGAAGCTGA 589
Db 519 AACTGAACCGGAGTGTGAGGCGCACTCCCAAGCAATCTTGAAGTGAAGCTGA 578
Qy 590 TGGATAGTGCAGAGCTGAGGCGCCCTGCCCCCAGCAAGTAACTCGGAGTCAAGCGCA 649
Db 579 TGGATAGTGCAGAGCTGAGGCGCCCTGCCCCCAGCAAGTAACTCGGAGTCAAGCGCA 638
Qy 650 CGTGCTACGAGGAGGCGGCGGCGCATGAGAGGCGCGCCCACTTACAGAGGATCATCG 709
Db 639 CGTGCTACGAGGAGGCGGCGGCGCATGAGAGGCGCGCCCACTTACAGAGGATCATCG 698
Qy 710 GCCACTACCGGAGGCTCTCTTCCAGAGCAAGAGAGGCGCGCTTCTTGTGCG 769
Db 699 GCCACTACCGGAGGCTCTCTTCCAGAGCAAGAGAGGCGCGCTTCTTGTGCG 758
Qy 770 AGGGGAGCCCGCTTCCAGAGCAAGAGAGGCGCGCTTGAAGAGCGCATCTGAGCA 829
Db 759 AGGGGAGCCCGCTTCCAGAGCAAGAGAGGCGCGCTTGAAGAGCGCATCTGAGCA 818
Qy 830 AAGAGAGATTAACAGAAAGAGACCCCTCTC 861
Db 819 AAGAGAGATTAACAGAAAGAGACCCCTCTC 850

RESULT 13
US-10-205-823-412
; Sequence 412, Application US/10205823
; Publication No. US20030108963A1
; GENERAL INFORMATION:
; APPLICANT: Schlegel, Robert
; APPLICANT: Monahan, John E.
; APPLICANT: Endege, Wilson O.
; APPLICANT: Gannavarepu, Manjula
; APPLICANT: Gorbacheva, Bella
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Kamackar, Subhangl
; APPLICANT: Monsey, Angela M.
; APPLICANT: Glact, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Anderson, Dustin
; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
; TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
; TITLE OF INVENTION: THERAPY OF PROSTATE CANCER
; FILE REFERENCE: MRI-044
; CURRENT APPLICATION NUMBER: US/10/205, 823
; CURRENT FILING DATE: 2002-07-25
; PRIOR APPLICATION NUMBER: 60/307, 982
; PRIOR FILING DATE: 2001-07-25
; PRIOR APPLICATION NUMBER: 60/314, 356
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/325, 020
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: 60/341, 746
```

```
; PRIOR FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: 60/362, 158
; PRIOR FILING DATE: 2002-03-05
; NUMBER OF SEQ. ID NOS: 455
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ. ID NO 412
; LENGTH: 1141
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-205-823-412

Query Match      87.3%; Score 752; DB 15; Length 1141;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 110 CGAGAGCTGAGAGTTTTCATCATCATCATCTGTGTGTGTGTGTGTGTGTGTG 169
Db 100 CGAGAGCTGAGAGTTTTCATCATCATCATCTGTGTGTGTGTGTGTGTGTGTG 159
Qy 170 TGAATCAGTGTCTGTGAGGCACTTACAGAGTGTGTGTGTGTGTGTGTGTGTG 229
Db 160 TGAATCAGTGTCTGTGAGGCACTTACAGAGTGTGTGTGTGTGTGTGTGTGTG 219
Qy 230 GCCAGGGGCGAGAGAGAGAGATGCTCTGTCTTCAAGAGATGCTGTGCTTCAAGAG 289
Db 220 GCCAGGGGCGAGAGAGAGAGATGCTCTGTCTTCAAGAGATGCTGTGCTTCAAGAG 279
Qy 290 GCACAGTGTCAAGGAGAGAGAAATCCCAAGGCGGAGGTCTAGAGCCGCCCTCGGCCACCG 349
Db 280 GCACAGTGTCAAGGAGAGAGAAATCCCAAGGCGGAGGTCTAGAGCCGCCCTCGGCCACCG 339
Qy 350 ACCGCTGAGCGGTGCGCCCTTCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCACT 409
Db 340 ACCGCTGAGCGGTGCGCCCTTCCAGCGGAGCGCTTCCAGCGCTTCCAGCGCACT 399
Qy 410 ATCCGTAAGCTGACAGAGATGCACTGCACTCCATCTGCTGTGAGACGGGAGG 469
Db 400 ATCCGTAAGCTGACAGAGATGCACTGCACTCCATCTGCTGTGAGACGGGAGG 459
Qy 470 AGCCCCCACTTACAGAGGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCACTG 529
Db 460 AGCCCCCACTTACAGAGGCGCTTCCAGCGCTTCCAGCGCTTCCAGCGCACTG 519
Qy 530 AACTGAACCGGAGTGTGAGGCGCACTCCCAAGCAATCTTGAAGTGAAGCTGA 589
Db 520 AACTGAACCGGAGTGTGAGGCGCACTCCCAAGCAATCTTGAAGTGAAGCTGA 579
Qy 590 TGGATAGTGCAGAGCTGAGGCGCCCTGCCCCCAGCAAGTAACTCGGAGTCAAGCGCA 649
Db 580 TGGATAGTGCAGAGCTGAGGCGCCCTGCCCCCAGCAAGTAACTCGGAGTCAAGCGCA 639
Qy 650 CGTGCTACGAGGAGGCGGCGGCGCATGAGAGGCGCGCCCACTTACAGAGGATCATCG 709
Db 640 CGTGCTACGAGGAGGCGGCGGCGCATGAGAGGCGCGCCCACTTACAGAGGATCATCG 699
Qy 710 GCCACTACCGGAGGCTCTCTTCCAGAGCAAGAGAGGCGCGCTTCTTGTGCG 769
Db 700 GCCACTACCGGAGGCTCTCTTCCAGAGCAAGAGAGGCGCGCTTCTTGTGCG 759
Qy 770 AGGGGAGCCCGCTTCCAGAGCAAGAGAGGCGCGCTTGAAGAGCGCATCTGAGCA 829
Db 760 AGGGGAGCCCGCTTCCAGAGCAAGAGAGGCGCGCTTGAAGAGCGCATCTGAGCA 819
Qy 830 AAGAGAGATTAACAGAAAGAGACCCCTCTC 861
Db 820 AAGAGAGATTAACAGAAAGAGACCCCTCTC 851

RESULT 14
US-10-301-822-208
; Sequence 208, Application US/10301822
; Publication No. US20030148410A1
; GENERAL INFORMATION:
```



```
Db      ||||||| 520 AACTGAACCGGAGTCGTCGCGCACCCCAACAGAACATCTTGACAGTGACCTGA 579
QY      ||||||| 590 TGGATAGTGCAGGCTGGCGGCGCCCTGACCCCCACAGAGTAACTCGGGCATGACGCCA 649
Db      ||||||| 580 TGGATAGTGCAGGCTGGCGGCGCCCTGACCCCCACAGAGTAACTCGGGCATGACGCCA 639
QY      ||||||| 650 CGTGCTACGCGCAGCGCGGCGGCGCATGAGAGGGGCGCCCACTACAGCGAGTCAATCG 709
Db      ||||||| 640 CGTGCTACGCGCAGCGGCGGCGCATGAGAGGGGCGCCCACTACAGCGAGTCAATCG 699
QY      ||||||| 710 GCCACTACCGCGGCTCTCTTCCAGCACAACAGAGAGTGGGCGCCCTCTTGCTGG 769
Db      ||||||| 700 GCCACTACCGCGGCTCTCTTCCAGCACAACAGAGAGTGGGCGCCCTCTTGCTGG 759
QY      ||||||| 770 AGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGGCGAGCCATCTGAGCA 829
Db      ||||||| 760 AGGGGACCGGCTCCACACACACATCGCGCCCTAGAGAGGCGAGCCATCTGAGCA 819
QY      ||||||| 830 AAGAGAAGATTAACAGAAAGACACCCCTCTC 861
Db      ||||||| 820 AAGAGAAGATTAACAGAAAGACACCCCTCTC 851
```

Search completed: February 20, 2005, 02:39:13
Job time : 485.77 secs

This Page Blank (uspto)

1	693	80.5	901	3	CR612083	CR612083 full-1 Leng
2	614	71.3	967	5	B0641849	B0641849 AGENCCOURT
3	566	65.7	1046	5	BM922276	BM922276 AGENCCOURT
4	558	64.8	609	5	B0636742	B0636742 hpl1306-X-Y
5	550	63.9	551	4	BM141979	BM141979 f:ES211-Y
6	536	62.3	551	4	CV028567	CV028567 7115 Full1
7	511	59.3	850	5	B0602918	B0602918 AGENCCOURT
8	499	58.0	916	5	B0954555	B0954555 AGENCCOURT
9	497	57.7	890	5	B0690750	B0690750 AGENCCOURT
c 10	485	56.3	850	1	AL558881	AL558881 AL558881
c 11	474	55.1	572	5	BX641317	BX641317 DXF206866
c 12	470	54.6	729	5	B0575741	B0575741 UT-H-B21-
13	449	52.1	945	5	B0538219	B0538219 AGENCCOURT
14	439	51.0	787	9	AL419334	AL419334 Homo sapi
15	425	49.4	897	1	AL558882	AL558882 AL558882
c 16	424	49.2	1038	1	AL517150	AL517150 AL517150
c 17	420	48.8	655	5	B0691705	B0691705 AGENCCOURT
c 18	420	48.8	1280	5	B0691500	B0691500 AGENCCOURT
c 19	417	48.4	782	5	B0015170	B0015170 UT-H-ED1-
c 20	402	46.7	964	5	B0859860	B0859860 AGENCCOURT
c 21	394	45.8	602	6	CA431191	CA431191 UT-H-FG1-
c 22	393	45.6	461	4	BM712680	BM712680 UT-E-BJ0-
c 23	390	45.3	933	5	B0169156	B0169156 AGENCCOURT
c 24	389	45.2	673	4	BM714472	BM714472 UT-E-BJ0-

C	25	380	44.1	588	5	B0624784	UI-H-FGI-
	26	374	43.4	844	5	B0686793	AGENCYCOURT
	27	374	43.4	938	5	BUI57842	AGENCYCOURT
	28	374	43.4	952	5	BUI57855	AGENCYCOURT
C	29	369	44.9	559	2	BEB55409	AGENCYCOURT
C	30	369	42.9	629	5	BUI730650	UI-E-CII-
	31	358	41.6	1127	5	BUI74654	AGENCYCOURT
C	32	353	41.0	730	4	BM677662	UI-E-EOI-
C	33	351	40.8	626	5	BM6774396	UI-CF-ECI
	34	347	40.3	544	7	CN296134	AGENCYCOURT
C	35	345	40.1	728	5	BUE83523	UI-CF-ECI
	36	335	38.9	570	5	B0575582	UI-H-EZI-
C	37	331	38.4	899	5	BUI96912	AGENCYCOURT
	38	330	38.3	552	4	BM713900	UI-E-EJO-
C	39	329	38.2	563	6	CB049800	NISC_gj13
	40	302	35.1	651	6	CB554226	CBSP50052
C	41	302	35.1	693	1	A1761441	wg55E07_x
C	42	300	34.8	646	5	BUB59841	AGENCYCOURT
C	43	290	33.7	867	5	BX362296	EX362396
C	44	279	32.4	547	4	BM676516	UI-E-EJO-
C	45	277	32.2	577	6	CB108549	K-EST0148

ALIGNMENTS

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES	ORIGIN
CR612083	901 bp. mRNA. linear. HTC 21-JUL-2004	CR612083	1	GI:50492890	HTC; CNSLT. cDNA.	Homo sapiens (human)	Full-length cDNA clone CS0D015YF12 of T cells (Jurkat cell line). Cot 10-normalized of Homo sapiens (human).					<p>Location/Qualifiers</p> <p>1..901</p> <p>/organism="Homo sapiens"</p> <p>/mol_type="mRNA"</p> <p>/db_xref="taxon:9606"</p> <p>/clone="CS0D015YF12"</p> <p>/tissue_type="T cells (Jurkat cell line)"</p> <p>Cot 10-normalized"</p> <p>/plasmid="PCWVSPORT_6"</p>	<p>80.5%: Score 693; DB 3; Length 901;</p> <p>Best Local Similarity 100.0%; Pzed. NO. 0;</p> <p>Matches 693; Conservative 0; Mismatches 0; Indels 0; Gaps 0;</p>

```

Db      1  GTGATACAGTGCCTGCTGAGCCATCAAGCTGTCTGACGAGCTTCATCAGCCGGGAC 60
Qy      229 AGCCAGGGGGGAGAGAGAGATGCTGTCTCAGAGAGATGCTGTGGCCCTCGAG 288
Db      61  AGCCAGGGGGGAGAGAGAGATGCTGTCTCAGAGAGATGCTGTGGCCCTCGAG 120
Qy      289 AGCAGAGTGTCAAGGCAAGGAAATCCAGAGCCGAGGTCTACGCCCCCTCGAGCC 348
Db      121 AGCAGAGTGTCAAGGCAAGGAAATCCAGAGCCGAGGTCTACGCCCCCTCGAGCC 180
Qy      349 GAGCCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 408
Db      181 GAGCCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 240
Qy      409 TATCCGTACCTGACAGCAGATGCACTGTGCACCACTCATCTGTGTGTGTGTGTGTGT 468
Db      241 TATCCGTACCTGACAGCAGATGCACTGTGCACCACTCATCTGTGTGTGTGTGTGTGT 300
Qy      469 GAGCCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 528
Db      301 GAGCCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGG 360
Qy      529 GAATGTGAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 588
Db      361 GAATGTGAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 420
Qy      589 ATGATAGTGTGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 648
Db      421 ATGATAGTGTGCAGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy      649 AGTGTCTACGCGCAGCGGCGGCGCATGTGAGGGGCGCGCGCCATCAAGAGAGTATC 708
Db      481 AGTGTCTACGCGCAGCGGCGGCGCATGTGAGGGGCGCGCGCCATCAAGAGAGTATC 540
Qy      709 GGCCTACTACCGGCGGCTCTCTTCTTCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 768
Db      541 GGCCTACTACCGGCGGCTCTCTTCTTCAAGACAGAGAGAGAGAGAGAGAGAGAGAGAG 600
Qy      769 GAGGAGAGCCCGGCTTCAACACACACACACACACACACACACACACACACACACACAC 828
Db      601 GAGGAGAGCCCGGCTTCAACACACACACACACACACACACACACACACACACACACAC 660
Qy      829 AAAGAGAGATTAACAGAAAGACACCTCTCTC 861
Db      661 AAAGAGAGATTAACAGAAAGACACCTCTCTC 693

RESULT 2
BO641849 967 bp mRNA linear EST 15-JUN-2002
LOCUS AGENCOURT 8287174 NIH_MGC_43 Homo sapiens cDNA clone IMAGE:6292265
DEFINITION 5', mRNA sequence.
ACCESSION BO641849
VERSION BO641849.1 GI:21766021
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL Contact: Robert Strausberg, Ph.D.
COMMENT Email: sgabs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Rubin Laboratory
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/MLNL at:
http://image.llnl.gov
Plate: L1CM2493 row: g column: 18

```

```

FEATURES
SOURCE High quality sequence stop: 571.
Location/Qualifiers
1..967
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6292265"
/issue_type="normal pigmented retinal epithelium"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_43"
/Note="Organ: eye; Vector: pOT7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dt priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adaptor: GGACGAG(G). Library constructed by Ling Hong
in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC Library."

ORIGIN
Query Match 71.3%; Score 614; DB 5; Length 967;
Best Local Similarity 99.7%; Pred. No. 6.5e-298;
Matches 714; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      112 GAGCTGAGTTTGTTCAGATCATCATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 171
Db      1  GAGCTGAGTTTGTTCAGATCATCATCATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 60
Qy      172 ATGACGTGCTGCTGAGCCATCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 231
Db      61 ATGACGTGCTGCTGAGCCATCAAAAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 120
Qy      232 CAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 291
Db      121 CAGGGGCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
Qy      292 ACAGTGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 351
Db      181 ACAGTGTCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCA 240
Qy      352 CGCTTGGCGGTGCGGCTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 411
Db      241 CGCTTGGCGGTGCGGCTTGTGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
Qy      412 CCGTACCTGACAGACAGATTCAGCTGACCTGACCAACCAATCTGCTGTCAAGCGGGAGAG 471
Db      301 CCGTACCTGACAGACAGATTCAGCTGACCTGACCAACCAATCTGCTGTCAAGCGGGAGAG 360
Qy      472 CCCCACCTTACAGAGGCGCTTGCACCTTCAAGCTTGGGAGCCCGAGAGAGAGAGAGAG 531
Db      361 CCCCACCTTACAGAGGCGCTTGCACCTTCAAGCTTGGGAGCCCGAGAGAGAGAGAGAG 420
Qy      532 CTGAAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 591
Db      421 CTGAAACCGGAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 480
Qy      592 GATATGTCCAGAGGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 651
Db      481 GATATGTCCAGAGGTGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
Qy      652 TGTCTACGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 711
Db      541 TGTCTACGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 600
Qy      712 CACTTACCGGCGGCTTCTTCTTCAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 771
Db      601 CACTTACCGGCGGCTTCTTCTTCAAGACACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
Qy      772 GGGAGCCGCGCTCACACACACACATGTGGCGGCTTGAAGAGGAGGAGGAGGAGGAGGAG 827
Db      661 GGGAGCCGCGCTCACACACACACATGTGGCGGCTTGAAGAGGAGGAGGAGGAGGAGGAG 716

```

Dn		367	GGCAACGGAATCCAGAGCGCAGGTCTAAGCCCCGCCTGGGCCAACGACCGCTT93CC	426
Oy		361	GTCGCCGCCCTTGCGCCAGCGGAGCGCTTCCACCGCTTCCAGCCCACTGATCGTACTG	420
Dd		427	GTGCCGCCCTTGCGCCAGCGGAGCGGCTTCCACCGCTTCCAGCCCACTGATCGTACTG	486
Oy		421	CAGACAAGATTCGACCTGCGACCACCATCTGCTGTCAGACGGGAGAGACCCCAACC	480
Dd		487	CAGACAAGATTCGACCTGCGACCACCATCTGCTGTCAGACGGGAGAGACCCCAACC	546
Oy		481	TACCAAGGAGCCCTTCACCTTCAGCTTCGGGACCCCGAGCAGAGCTGGAAGTAACCGG	540
Dd		547	TACCAAGGAGCCCTTCACCTTCAGCTTCGGGACCCCGAGCAGAGCTGGAAGTAACCGG	606
Oy		541	GAGTCGGTGGCGCGACCCCAAACAGAACCATTCTTGACAGTAGTGAATGATGACC	600
Dd		607	GAGTCGGTGGCGCGACCCCAAACAGAACCATTCTTGACAGTAGTGAATGATGACC	666
Oy		601	AGGCTGGGCGGCGCCCTTGCGCCCCCGACAGATTAATCTCGGGCATCAGCGCACTGTAACGC	660
Dd		667	AGGCTGGGCGGCGCCCTTGCGCCCCCGACAGATTAATCTCGGGCATCAGCGCACTGTAACGC	726
Oy		661	AGCGGCGG 668	
Dd		727	AGCGGCGG 734	
RESULT 4				
B0636742				
LOCUS		609 bp	mRNA	linear EST 15-JUL-2002
DEFINITION		hd13h06.v1 Human Retina cDNA (Un-normalized, unamplified): hd/he		
ACCESSION		B0636742		
VERSION		B0636742.1		
KEYWORDS		EST.		
SOURCE		Homo sapiens (human)		
ORGANISM		Homo sapiens		
		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
		Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
		1 (bases 1 to 609)		
REFERENCE		Wistow,G., Bernstein,S.L., Watt,M.K., Ray,S., Behal,A.,		
AUTHORS		Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.		
		Expressed sequence tag analysis of human retina for the NEIBank		
		Project: Rebinding, an abundant, novel retinal cDNA and alternative		
		splicing of other retina-preferred gene transcripts		
		Mol. Vis. 8 (4), 196-204 (2002)		
JOURNAL		22103461		
MEDLINE		12107411		
PUBMED		Contact: Wistow G		
COMMENT		Section on Molecular Structure and Function		
		National Eye Institute		
		6/331, NIH, Bethesda, MD 20892-2740, USA		
		Tel: 301 402 3452		
		Fax: 301 496 0078		
		Email: graeme@helix.nih.gov		
		Plate: 13 row: h column: 06		
		Seq primer: M13RPL reverse primer (ABI).		
FEATURES		Location/Qualifiers		
Source		1..609		
		/organism="Homo sapiens"		
		/mol_type="mRNA"		
		/db_xref="taxon:9606"		
		/clone="hd13h06"		
		/tissue_type="Retina"		
		/dev_stage="Adult"		
		/lab_host="EMDHI0B"		
		/clone_id="Human Retina cDNA (Un-normalized,		
		unamplified): hd/he"		
		/note="Organ: Eye; Vector: pSPORT1; Neural retina tissue		
		was dissected from two 80 year old donors with no observed		
		eye disease. 100ug of total RNA was used for library		
		construction. A directional cloned cDNA library in the		
		pSPORT1 vector (Life Technologies) was constructed at		

Bioserve Biotechnology (Laurel MD) essentially following the protocols of the SuperScript Plasmid System full details of which are contained in the manufacturer's instruction manual (<http://www.lifetech.com/>). First strand synthesis was carried out using a Not I primer-adaptor (5'-pGACTAGTCTAGATTCGGACGGCGCC(T)15-3'). EST analysis was performed on the unamplified library at the NIH Intramural Sequencing Center (NISC)."

ORIGIN

```

Query Match      64.8%; Score 1558; DB 5; Length 609;
Best Local Similarity 99.8%; Pred. No. 1.1e-269;
Matches 608; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 219 CAGCCGCGACAGCCGAGGCGGAGAGAGATGCTGCTGAGAGAGATGCTGCTG 278
DB 1 CAGCCGCGACAGCCGAGGCGGAGAGAGATGCTGCTGAGAGAGATGCTGCTG 60
QY 279 GCGCTCGAGAGACAGAGTGTCTAGGACGGAATCCGAGAGCGGAGGTCTAGCGCCG 338
DB 61 GCGCTCGAGAGACAGAGTGTCTAGGACGGAATCCGAGAGCGGAGGTCTAGCGCCG 120
QY 339 TCGGCGCGACCGAGCGGCTGCGCTGCGCTGCGCTGCGCGGAGAGCGCTTCCACGCTT 398
DB 121 TCGGCGCGACCGAGCGGCTGCGCTGCGCTGCGCTGCGCGGAGAGCGCTTCCACGCTT 180
QY 399 CAGGCGCGACCGAGCGGCTGCGCTGCGCTGCGCTGCGCGGAGAGCGCTTCCACGCTT 458
DB 181 CAGGCGCGACCGAGCGGCTGCGCTGCGCTGCGCTGCGCGGAGAGCGCTTCCACGCTT 240
QY 459 AGAGCGGCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 518
DB 241 AGAGCGGCGAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 300
QY 519 GCGAGAGCTGAGACTGAGACCGGAGAGTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGG 578
DB 301 GCGAGAGCTGAGACTGAGACCGGAGAGTGGTGGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 579 CAGTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 638
DB 361 CAGTGAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
QY 639 CATAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 698
DB 421 CATAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
QY 699 CGAGAGTATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 758
DB 481 CGAGAGTATGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 759 CTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 818
DB 541 CTCTCTGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 600
QY 819 CATCTGGAG 827
DB 601 CATCTGGAG 609

```

```

RESULT 5
BM141979      551 bp      mRNA      linear      EST 12-MAR-2002
LOCUS         1425a11.y1 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
DEFINITION    cDNA clone IMAGE:5677341 5' similar to TR:Q9UJD3 Q9UJD3 D718J7.1
              // mRNA sequence.
ACCESSION     BM141979
VERSION       BM141979.1 GI:17152046
KEYWORDS      EST.
SOURCE        Homo sapiens (human)
ORGANISM      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

REFERENCE

1 (bases 1 to 551)
 Melton, D., Brown, J., Keny, G., Permutt, A., Lee, C., Kaestner, K.,
 Lemishka, I., Scarce, M., Brestelli, J., Gradwohl, G., Clifton, S.,
 Hillier, D., Maira, D., Pape, D., Wylie, T., Martin, J., Blistain, A.,
 Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
 Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarishvili, R.,
 Williams, T., Jackson, Y., and Bowers, Y.
 Endocrine Pancreas Consortium
 Unpublished (2000)

TITLE

Endocrine Pancreas Consortium
 Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
 MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@ionh.harvard.edu

COMMENT

Library was constructed by Dr. Douglas Melton DNA sequencing by:
 Washington University Genome Sequencing Center for information on
 obtaining a clone please contact: Juliana Brown
 (brown@fas.harvard.edu) This sequence now available from the IMAGE
 Consortium, for clone orders contact: info@image.llnl.gov
 Seq primer: -40RP from Gibco
 High quality sequence stop: 429.
 Location/Qualifiers

FEATURES

source

```

1..551
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5677341"
/sex="Both"
/issue_type="Islets of Langerhans"
/dev stage="Adult"
/lab host="DH10B"
/clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
/note="Organ: Pancreas; Vector: pSPORT1; Site 1: Not 1;
Site 2: Sal 1; Starting library constructed using
Superscript library kit (Life Technologies). cDNA
made by oligo-dT priming. Size-selected by column
fractionation; average insert size 1.08 kb. Library was
amplified once on solid support and plasmid DNA from
library was prepared. The library DNA was normalized by
method #4 from Bonaldo, Lennon, and Soares 1996 Genome
Research 6:791-806; 0.5 microgram single-stranded library
plasmid DNA was mixed with 5 micrograms PCR product
representing library inserts and hybridized to an EcoT of
20. Single-stranded (unhybridized) plasmids were isolated
by hydroxyapatite chromatography and used to make this
library."

```

ORIGIN

```

Query Match      63.9%; Score 550; DB 4; Length 551;
Best Local Similarity 100.0%; Pred. No. 1.2e-265;
Matches 550; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 302 GCAACGGAATCCAGAGCGGAGGTCTACGCGCGCTGCGCCACGAGCGCTGGCGG 361
DB 1 GCAACGGAATCCAGAGCGGAGGTCTACGCGCGCTGCGCCACGAGCGCTGGCGG 60
QY 362 TGGCGCGCTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 421
DB 61 TGGCGCGCTTGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 422 AGCAGAGTGTGAGCTGTGACCAACCATCTGTGTGAGAGGAGGAGGAGGAGGAGG 481
DB 121 AGCAGAGTGTGAGCTGTGACCAACCATCTGTGTGAGAGGAGGAGGAGGAGGAGG 180
QY 482 ACCAGGCGCGCTGTGACCTTCCAGCTTGGAGACCCGAGCAGCAGCTGGAATGAACCGG 541
DB 181 ACCAGGCGCGCTGTGACCTTCCAGCTTGGAGACCCGAGCAGCAGCTGGAATGAACCGG 240
QY 542 AGTGGTGGCGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 601

```


ORIGIN	Query Match	62.3%;	Score 536;	DB 7;	Length 605;
	Best Local Similarity	99.8%;	Prod. No. 1.4e-258;		
	Matches 586;	Conservative 0;	Mismatches 1;	Indels 0;	Gaps 0;
OY	165	GGTGTGATCATCGTGCCTGCTGAGCCACTAACAAGCTGTGTGACAGGTCCTTCATCAGCCG	224		
Db	15	GGTGTGATCATCGTGCCTGCTGAGCCACTAACAAGCTGTGTGACAGGTCCTTCATCAGCCG	74		
OY	225	GCACAGCCAGGGGGCGAGAGAGAAATGCCCTTGTCTCAGAGAGATGCTGTGGCCCTC	284		
Db	75	GCACAGCCAGGGGGCGAGAGAGAAATGCCCTTGTCTCAGAGAGATGCTGTGGCCCTC	134		
OY	285	GGAGAGCAAGTGTCAAGGCAACGGAAATCCAGAGCCGCAAGGTCTAAGCCCGCCCTCGCCG	344		
Db	135	GGAGAGCAAGTGTCAAGGCAACGGAAATCCAGAGCCGCAAGGTCTAAGCCCGCCCTCGCCG	194		
OY	345	CACCGACCGGCTGGCCGCTGCGCCCTTCGACCAGCGGAGCGCTTTCACAGCTTTCAGCC	404		
Db	195	CACCGACCGGCTGGCCGCTGCGCCCTTCGACCAGCGGAGCGCTTTCACAGCTTTCAGCC	254		
OY	405	CACCTATTCGTAAGCTGAGCAAGAGATGACTGTCACCAACCAATCTTGCTGTGACAGCG	464		
Db	255	CACCTATTCGTAAGCTGAGCAAGAGATGACTGTCACCAACCAATCTTGCTGTGACAGCG	314		
OY	465	GGAGAGACCCCTCAACCTTCAAGAGGCCCCCTGCAACCTTCAGCTTGGGAAACCCGAGAGCA	524		
Db	315	GGAGAGACCCCTCAACCTTCAAGAGGCCCCCTGCAACCTTCAGCTTGGGAAACCCGAGAGCA	374		
OY	525	GCTGGAATCTGAAACCGGAGATCGGTCGCGACGCAACCCCAAGAGCAATCTTTCAGAGTGA	584		
Db	375	GCTGGAATCTGAAACCGGAGATCGGTCGCGACGCAACCCCAAGAGCAATCTTTCAGAGTGA	434		
OY	585	CCTGATGATATAGTGCAGGCTGGGCGGCCCTCTGCCCCCGACAGATATCTTGCGGCATTCAG	644		
Db	435	CCTGATGATATAGTGCAGGCTGGGCGGCCCTCTGCCCCCGACAGATATCTTGCGGCATTCAG	494		
OY	645	CGCCACGTGCTACGCGCAGCGCGCGGCGCATATGAGAGGGGCGCGCGCCACCTTACACAGAGT	704		
Db	495	CGCCACGTGCTACGCGCAGCGCGCGGCGCATATGAGAGGGGCGCGCGCCACCTTACACAGAGT	554		
OY	705	CATCGGCGCACTAACCGGGGATCTCTCTTCGAGCAACAGAGAGCAGTG	751		
Db	555	CATCGGCGCACTAACCGGGGATCTCTCTTCGAGCAACAGAGAGCAGTG	601		
RESULT 7	BU602918	850 bp	mRNA	linear	EST 20-SEP-2002
LOCUS	AGENCOURT_10016502 NIH_MGC_142 Homo sapiens cDNA clone				
DEFINITION	IMAGE:6497853 5', mRNA sequence.				
ACCESSION	BU602918				
VERSION	BU602918.1 GI:23254677				
KEYWORDS	BST.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eumetazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
REFERENCE	1 (bases 1 to 850)				
AUTHORS	NIH-MGC http://mgc.nci.nih.gov/				
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)				
JOURNAL	Unpublished (1999)				
COMMENT	Contact: Robert Strausberg, Ph. D.				
	Email: cgabs-remail.nih.gov				
	Tissue Procurement: NCI				
	CDNA Library Preparation: Michael Brownstein Laboratory				
	CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIMU)				
	DNA Sequencing by: Agencourt Bioscience Corporation				

QY 181 CTGCTGAGCCACTACAGCTGTCTGACGGTCTTTCATCAGCCGACAGCCAGGAGGCGG 240
 DB 250 CTGCTGAGCCACTACAGCTGTCTGACGGTCTTTCATCAGCCGACAGCCAGGAGGCGG 309
 QY 241 AGAGAGAGAGATGCTCTGTCTCTCAGAGAGATGCTGTGGCCCTTGAGAGACAGTGTCA 300
 DB 310 AGAGAGAGAGATGCTCTGTCTCTCAGAGAGATGCTGTGGCCCTTGAGAGACAGTGTCA 369
 QY 301 GGCAGAGAGATGCTCTGTCTCTCAGAGAGATGCTGTGGCCCTTGAGAGACAGTGTCA 360
 DB 370 GGCAGAGAGATGCTCTGTCTCTCAGAGAGATGCTGTGGCCCTTGAGAGACAGTGTCA 429
 QY 361 GTGCGCCCTTCTGCGCCAGCGGAGGAGCTTTCAGCGCTTTCAGCCCACTATCCGTACCTG 420
 DB 430 GTGCGCCCTTCTGCGCCAGCGGAGGAGCTTTCAGCGCTTTCAGCCCACTATCCGTACCTG 489
 QY 421 CAGCAGAGATGACCTGTGACACCAACCATCTGCTGTGACAGCGGAGAGAGCCGCCACCC 480
 DB 490 CAGCAGAGATGACCTGTGACACCAACCATCTGCTGTGACAGCGGAGAGAGCCGCCACCC 549
 QY 481 TACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
 DB 550 TACCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 609
 QY 541 GAGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
 DB 610 GAGTCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 669
 QY 601 A 601
 DB 670 A 670

RESULT 9
 B0690750 890 bp mRNA linear EST 15-JUL-2002
 LOCUS AGENCOURT 8046394 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6209341
 DEFINITION 5', mRNA sequence.
 ACCESSION B0690750
 VERSION B0690750.1 GI:21816066
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 890)
 NIH-MGC http://mgi.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Rubin Laboratory
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.lnl.gov
 Plate: LCM2368 row: h column: 14
 High quality sequence stop: 627.
 Location/Qualifiers
 1..890
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6209341"
 /issue_type="ductal carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_id="NIH_MGC_110"
 /note="Organ: pancreas; Vector: pOTB7; site: 1: XhoI;
 site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the

FEATURES
 source

following 5' adaptor: GGCAAGAG(G). Library constructed by
 Ling Hong in the Laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

Query Match 57.7%; Score 497; DB 5; Length 890;
 Best Local Similarity 99.8%; Pred. No. 6.1e-239;
 Matches 547; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

ORIGIN
 QY 110 CGAGCTGAGAGTTGTTCAATCATCATCTGCTGTGATGATGATGATGATGATGATGATGATG 169
 DB 128 CGAGCTGAGAGTTGTTCAATCATCATCTGCTGTGATGATGATGATGATGATGATGATGATG 187
 QY 170 TGATCAAGTCCCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 229
 DB 188 TGATCAAGTCCCTGCTGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 247
 QY 230 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 289
 DB 248 GCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 307
 QY 290 GCACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 349
 DB 308 GCACAGTGTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 367
 QY 350 ACCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 409
 DB 368 ACCGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 427
 QY 410 ATCCGTACTGACAGCAGAGATGACCTGACACCACTATCTGCTGTGATGATGATGATGATGATG 469
 DB 428 ATCCGTACTGACAGCAGAGATGACCTGACACCACTATCTGCTGTGATGATGATGATGATGATG 487
 QY 470 AGCCCCACCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 529
 DB 488 AGCCCCACCTTACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 547
 QY 530 AACTGAACCGGAGAGTCCGTGCGGACACCCCAACAGAACCATCTTGTGAAGTGAACCTGA 589
 DB 548 AACTGAACCGGAGAGTCCGTGCGGACACCCCAACAGAACCATCTTGTGAAGTGAACCTGA 607
 QY 590 TGATAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 649
 DB 608 TGATAGTGCAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 667
 QY 650 CGTGCTAC 657
 DB 668 CGTGCTAC 675

RESULT 10
 AL558881/c 850 bp mRNA linear EST 02-APR-2004
 LOCUS AL558881 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED
 DEFINITION Homo sapiens cDNA clone CS0D015F12 3-PRIME, mRNA sequence.
 ACCESSION AL558881
 VERSION AL558881.3 GI:46184268
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 850)
 L.I.W.B., Gruber, C., Jesse, J. and Polayres, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31283014.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 9945.r

For more information about this cluster, see
<http://www.genoscope.crs.fr/cdnaf?c=CS0D015D06NP1&c=9945.r>.

FEATURES
source

1. 850
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0D015YF12"
/cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
/note="1st strand cDNA was primed with a NotI-oligo (dt) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Query Match 56.3%; Score 485; DB 1; Length 850;

Best Local Similarity 99.4%; Pred. No. 6.9e-233; Matches 685; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```
OY 173 TCACGTGCTCTGAGCCATCAAGCTGTGACGGCTCTCATACGCGGACAGCC 232
DB 173 TCACGTGCTCTGAGCCATCAAGCTGTGACGGCTCTCATACGCGGACAGCC 232
OY 846 TCAGTGTCTCTGAGCCATCAAGCTGTGACGGCTCTCATACGCGGACAGCC 787
DB 846 TCAGTGTCTCTGAGCCATCAAGCTGTGACGGCTCTCATACGCGGACAGCC 787
OY 233 AGGGGCGGAGAGAGAAAGATCCCTGCTTCAAGAGATGCTGCGCTCGAGAGCA 292
DB 233 AGGGGCGGAGAGAGAAAGATCCCTGCTTCAAGAGATGCTGCGCTCGAGAGCA 292
OY 786 AGGGGCGGAGAGAGAAAGATCCCTGCTTCAAGAGATGCTGCGCTCGAGAGCA 727
DB 786 AGGGGCGGAGAGAGAAAGATCCCTGCTTCAAGAGATGCTGCGCTCGAGAGCA 727
OY 293 CAGTGTCAAGGAGAGAGATCCCAAGCGCGAGTCTACGCGCTGCGCCACCGA 352
DB 293 CAGTGTCAAGGAGAGAGATCCCAAGCGCGAGTCTACGCGCTGCGCCACCGA 352
OY 726 CAGTGTCAAGGAGAGAGATCCCAAGCGCGAGTCTACGCGCTGCGCCACCGA 667
DB 726 CAGTGTCAAGGAGAGAGATCCCAAGCGCGAGTCTACGCGCTGCGCCACCGA 667
OY 353 GCCTGCGCGTCCGCGCTTCCGCGAGGAGCGCTTCAAGCGCTTCAAGCGCGA 412
DB 353 GCCTGCGCGTCCGCGCTTCCGCGAGGAGCGCTTCAAGCGCTTCAAGCGCGA 412
OY 666 GCCTGCGCGTCCGCGCTTCCGCGAGGAGCGCTTCAAGCGCTTCAAGCGCGA 607
DB 666 GCCTGCGCGTCCGCGCTTCCGCGAGGAGCGCTTCAAGCGCTTCAAGCGCGA 607
OY 413 CGTACTGACAGCAGAGATGACCTGCGCGCCACCTTCTGCTTCAAGCGGAGAG 547
DB 413 CGTACTGACAGCAGAGATGACCTGCGCGCCACCTTCTGCTTCAAGCGGAGAG 547
OY 473 CCGGACCGTACAGAGCGCGCTTCCGCGAGGAGCGCTTCAAGCGGAGAGAG 532
DB 473 CCGGACCGTACAGAGCGCGCTTCCGCGAGGAGCGCTTCAAGCGGAGAGAG 532
OY 546 CCGGACCGTACAGAGCGCGCTTCCGCGAGGAGCGCTTCAAGCGGAGAGAG 487
DB 546 CCGGACCGTACAGAGCGCGCTTCCGCGAGGAGCGCTTCAAGCGGAGAGAG 487
OY 533 TGAACCGGAGTGGTGGCGGACCGCCCAAGAGATCTTGAAGAGTGAAGTGG 592
DB 533 TGAACCGGAGTGGTGGCGGACCGCCCAAGAGATCTTGAAGAGTGAAGTGG 592
OY 486 TGAACCGGAGTGGTGGCGGACCGCCCAAGAGATCTTGAAGAGTGAAGTGG 427
DB 486 TGAACCGGAGTGGTGGCGGACCGCCCAAGAGATCTTGAAGAGTGAAGTGG 427
OY 593 ATAAGTGCAGAGTGGGCGGCGCTGCGCGCCAGAGATCTGCGGAGTCAAG 652
DB 593 ATAAGTGCAGAGTGGGCGGCGCTGCGCGCCAGAGATCTGCGGAGTCAAG 652
OY 426 ATAAGTGCAGAGTGGGCGGCGCTGCGCGCCAGAGATCTGCGGAGTCAAG 367
DB 426 ATAAGTGCAGAGTGGGCGGCGCTGCGCGCCAGAGATCTGCGGAGTCAAG 367
OY 653 GCTACCGGAGAGGCGGCGGAGTGAAGAGGCGCGCCCACTTACAGAGAGTCA 712
DB 653 GCTACCGGAGAGGCGGCGGAGTGAAGAGGCGCGCCCACTTACAGAGAGTCA 712
OY 366 GCTACCGGAGAGGCGGCGGAGTGAAGAGGCGCGCCCACTTACAGAGAGTCA 307
DB 366 GCTACCGGAGAGGCGGCGGAGTGAAGAGGCGCGCCCACTTACAGAGAGTCA 307
OY 713 ACTACCGGAGTCTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 772
DB 713 ACTACCGGAGTCTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 772
OY 306 ACTACCGGAGTCTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 247
DB 306 ACTACCGGAGTCTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 247
OY 773 GAGACCGGAGTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 832
DB 773 GAGACCGGAGTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 832
OY 246 GAGACCGGAGTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 187
DB 246 GAGACCGGAGTCTTCCAGACGAGAGAGATGAGGAGCGCGCTCTTGTGAG 187
OY 833 AGAAGATTAAGAGAGAGACCGCTCTC 861
```

DB 186 AGAAGATTAAGAGAGAGACCGCTCTC 158

RESULT 11

EX641317

LOCUS

DEFINITION DXFZp686K23134 r1 686 (synonym: hlc03) Homo sapiens cDNA clone

ACCESSION

EX641317

VERSION

EX641317

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CONTACT

MIPS

Ingolstaedter Landstr.1, D-85764 Neuberberg, Germany

This is the 5' sequence of the clone insert

Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ), Email: s.wiemann@dkfz-heidelberg.de;

Heidelberg/Germany) within the cDNA sequencing consortium of the

German Genome Project.

No sl sequence available.

This clone (DXFZp686K23134) is available at the RZPD in Berlin.

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059

Berlin-Charlottenburg, GERMANY; Email: clone@rzd.de.

Location/Qualifiers

1. 572

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="DXFZp686K23134"

/dev_stage="adult"

/lab_host="DH10B"

/clone_lib="686 (synonym: hlc03)"

/note="Vector: pTriplEx2; Site_1: SfiI; Site_2: SfiI; cDNA-collection"

ORIGIN

Query Match 55.1%; Score 474; DB 5; Length 572;

Best Local Similarity 99.8%; Pred. No. 2.4e-227; Matches 524; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
OY 258 GTCTTCAAGAGAGATGCTGTGCGCTTCCGAGAGAGAGAGAGAGAGTCA 317
DB 258 GTCTTCAAGAGAGATGCTGTGCGCTTCCGAGAGAGAGAGAGAGAGTCA 317
OY 1 GTCTTCAAGAGAGATGCTGTGCGCTTCCGAGAGAGAGAGAGAGAGTCA 60
DB 1 GTCTTCAAGAGAGATGCTGTGCGCTTCCGAGAGAGAGAGAGAGAGTCA 60
OY 318 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 377
DB 318 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 377
OY 61 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 120
DB 61 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 120
OY 378 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 437
DB 378 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 437
OY 121 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 180
DB 121 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 180
OY 438 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 497
DB 438 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 497
OY 181 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 240
DB 181 GCGGAGAGTCTTCAAGCGCGCTTCCGAGAGAGAGAGAGAGAGTCA 240
OY 498 CCTTCAGCTTCCGAGAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 557
DB 498 CCTTCAGCTTCCGAGAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 557
OY 241 CCTTCAGCTTCCGAGAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 300
DB 241 CCTTCAGCTTCCGAGAGAGAGAGAGAGAGTGAAGTGAAGTGAAGTGAAGTGA 300
```

QY 558 CCGAAACGAAACATCTTTCAGACGTGACCTGATGAGTCCAGGCTGCGGCGCCCTG 617
 Db 301 CCGAAACGAAACATCTTTCAGACGTGACCTGATGATGTCGACGCTGCGGCGCCCTG 360
 QY 618 CCCCCCGAGTACTCTGGGCTATGAGGCGACCTGCTACAGGCGGCGGCGGATGGA 677
 Db 361 CCCCCCGAGTACTCTGGGCTATGAGGCGACCTGCTACAGGCGGCGGCGGATGGA 420
 QY 678 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 737
 Db 421 GGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 480
 QY 738 CCGACGAGGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 782
 Db 481 CCGACGAGGAGTGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 525

RESULT 12
 B0575741/C
 LOCUS 729 bp mRNA linear EST 19-JUN-2002
 DEFINITION UI-H-E21-bbg-h-14-0-UI.s1 NCI CGAP Ch2 Homo sapiens CDNA clone
 UI-H-E21-bbg-h-14-0-UI 3', mRNA sequence.
 ACCESSION B0575741
 VERSION B0575741.1 GI:21479058
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 729)
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITL NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.
 COMMENT National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index

JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: Dr. Steven Gitelis/ Rush Presbyterian, Dept. of
 Orthopedics

CDNA library preparation: Dr. M. Bento Soares, University of Iowa
 CDNA library arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained
 from Dr. M. Bento Soares, bento-soares@iowa.edu
 Seq primer: M13 FORWARD
 POLYA=yes.

FEATURES
 SOURCE Location/Qualifiers

1..729
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-E21-bbg-h-14-0-UI"
 /tissue_type="Chondrosarcoma Grade II"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_lib="NCI CGAP Ch2"
 /note="Organ: Left Pelvis; Vector: pRTT3-Pac (pharmacia)
 with a modified polylinker; Site 1: Ecor I; Site 2: Not I;
 NCI CGAP Ch2 is a normalized CDNA library containing the
 following tissue(s): Chondrosarcoma Grade II. The library
 was constructed according to Bonaldo, Lennon and Soares,
 Genome Research, 6:791-806, 1996. First strand CDNA
 synthesis was primed with an oligo-dT primer containing a
 Not I site. Double stranded cDNA was ligated to an Ecor I
 adaptor, digested with Not I, and cloned directionally
 into pRTT3-Pac vector. The oligonucleotide used to prime
 the synthesis of first-strand CDNA contains a library tag
 sequence that is located between the Not I site and the
 (dfr)18 tail. The sequence tag for this library is
 TGATCAGCGT
 TAG_TISSUE=grade-2-chondrosarcoma
 TAG_LIB=UI-H-E21
 TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 54.6%; Score 470; DB 5; Length 729;
 Best Local Similarity 99.8%; Pred. No. 2.5e-225;
 Matches 520; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 341 GGGCCACCGACCGCGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 400
 Db 729 GGGCCACCGACCGCGCTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 670
 QY 401 AGCCCACTATCCGCTACCTGAGACGAGATGACCTGCGCACCCACATCTCGTGTAG 460
 Db 669 AGCCCACTATCCGCTACCTGAGACGAGATGACCTGCGCACCCACATCTCGTGTAG 610
 QY 461 ACGGGAG 520
 Db 609 ACGGGAG 550
 QY 521 AGCAGCTGGAACGTGACCGGAGAGTGGTGGCGGACCCCGCAACAGAACATCTTGA 580
 Db 549 AGCAGCTGGAACGTGACCGGAGAGTGGTGGCGGACCCCGCAACAGAACATCTTGA 490
 QY 581 GTGACCTGATGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 640
 Db 489 GTGACCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
 QY 641 TCAGCGCGACGCTGCTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 700
 Db 429 TCAGCGCGACGCTGCTACGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 370
 QY 701 AGGTGATCGGCGCTACCTACCGGAGGCTCTCTTCAGACACAGACAGAGAGAGAGAGAG 760
 Db 369 AGGTGATCGGCGCTACCTACCGGAGGCTCTCTTCAGACACAGAGAGAGAGAGAGAGAG 310
 QY 761 CTTGCTGAG 820
 Db 309 CTTGCTGAG 250
 QY 821 TCTGAGCAAAAGAGAGAGATTAACAGAAAGAGACACCTCTC 861
 Db 249 TCTGAGCAAAAGAGAGATTAACAGAAAGAGACACCTCTC 209

RESULT 13
 B0539219
 LOCUS 945 bp mRNA linear EST 13-SEP-2002
 DEFINITION AGENCOURT_10215265 NIH_MGC_107 Homo sapiens CDNA clone
 IMAG:6569922 5', mRNA sequence.
 ACCESSION B0539219
 VERSION B0539219.1 GI:22849660
 KEYWORDS EST.

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 945)
 AUTHORS Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Eukaryota; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 TITL NIH-MGC http://mgc.ncbi.nlm.nih.gov/
 JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
 COMMENT Unpublished (1999)

CDNA library preparation: Rubin Laboratory
 CDNA library arrayed by: The I.M.A.G.E. Consortium (LNL)
 DNA sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNL at:
 http://image.llnl.gov
 Plate: LICM2757 row: p column: 18
 High quality sequence, stop: 663.

FEATURES
 SOURCE Location/Qualifiers
 1..945
 /organism="Homo sapiens"
 /mol_type="mRNA"

Homo sapiens cDNA clone CS0DJ015YF12 5-PRIME, mRNA sequence.
 AL558882
 VERSION AL558882.3 GI:46184269
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 897)
 L.I.W.B., Gruber, C., Jesssee, J. and Polayes, D.
 Pull-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31283015.
 COMMENT
 Genoscope - Centre National de Sequencage
 2 rue Gaston Cremieux, CP 5706 - 91057 Evry cedex - FRANCE
 Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 9945.1
 For more information about this cluster, see
 http://www.genoscope.cns.fr/cdna?ts=CS0DJ015DC06P1&c=9945.1.
 Location/Qualifiers
 1..897
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CS0DJ015YF12"
 /cell_type="T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED"
 /cell_line="JURKAT"
 /clone_lib="Homo sapiens T CELLS (JURKAT CELL LINE) COT
 10-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo (dT)
 primer. Five prime end enriched, double-strand cDNA was
 digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

ORIGIN

Query Match 49.4%; Score 425; DB 1; Length 897;
 Best Local Similarity 99.5%; Pred. No. 1.2e-202;
 Matches 645; Conservative 0; Mismatches 2; Indels 1; Gaps 1;
 169 GTGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGCTCTTCATCAGCCGGCAC 228
 1 GTGATCAGTGCCTGCTGAGCCACTACAGCTGTCTGACGCTCTTCATCAGCCGGCAC 60
 229 AGCCAGGGGGGAGAGAGAAAGATGCCCTGTCTCAGAGGATGCCCTGGGCGCTCGGAG 288
 61 AGCCAGGGGGGAGAGAGAAAGATGCCCTGTCTCAGAGGATGCCCTGGGCGCTCGGAG 120
 289 AGCAGAGTGTCAAGCAAGCAAGATCCAGAGCCGAGGCTTACGCCCGCTCGGCCACC 348
 121 AGCAGAGTGTCAAGCAAGCAAGATCCAGAGCCGCA-GTCTACGCCCGCTCGGCCACC 179
 349 GACCGCTGCGCGCTGCGCCCTTGCCTCAGAGGAGCGCTTCCACCGCTTCAGCCACC 408
 180 GACCGCTGCGCGCTGCGCCCTTGCCTCAGAGGAGCGCTTCCACCGCTTCAGCCACC 239
 409 TATCCGTAAGTCAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 468
 240 TATCCGTAAGTCAAGCAAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAG 299
 469 GAGCCCAACCTTCAAGGAGCCCTGACCTTCAGCTTCGAGAGCCCGGAGCAGAGCTG 528
 300 GAGCCCAACCTTCAAGGAGCCCTGACCTTCAGCTTCGAGAGCCCGGAGCAGAGCTG 359
 529 GAACTGAACCGGAGTGTGTGCGGCAACCCCAAAAGAAACATCTTGAAGTACCTG 588
 360 GAACTGAACCGGAGTGTGTGCGGCAACCCCAAAAGAAACATCTTGAAGTACCTG 419

QY 589 ATGATATGTCACAGCTGAGCGGCGCCCTGCCCCCAGCAGTAACTGGGCAATCAGCGCC 648
 DB 420 ATGATATGTCACAGCTGAGCGGCGCCCTGCCCCCAGCAGTAACTGGGCAATCAGCGCC 479
 QY 649 ACGTCTACAGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 708
 DB 480 ACGTCTACAGGACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 539
 QY 709 GGCCTACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 768
 DB 540 GGCCTACACCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 599
 QY 769 GAGGGAGCCCGGCTCCACACACACACACACACATCGCGCCCTTAGAGAGCGCA 816
 DB 600 GAGGGAGCCCGGCTCCACACACACACACACACATCGCGCCCTTAGAGAGCGCA 647

Search completed: February 19, 2005, 23:58:34
 Job time : 2710.09 secs

This Page Blank (uspto)